

COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-276-852-35

Query Match 4.3%; Score 18; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGGAGAGCCACCGCCAC 84
|||||
DB 31 ATGGAGAGCCACCGCCAC 14

RESULT 3
US-08-133-011-107/c
Sequence 107, Application US/08133011
Patent No. 5658727
GENERAL INFORMATION:
APPLICANT: Kang, Angray
APPLICANT: Barbas, Carlos
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
TITLE OF INVENTION: PHAGEMIDS
NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5658727th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,011
FILING DATE: 08-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-133-011-107

Query Match 4.3%; Score 18; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGGAGAGCCACCGCCAC 84
|||||
DB 31 ATGGAGAGCCACCGCCAC 14

RESULT 4
US-08-322-730A-107/c
Sequence 107, Application US/08322730A
Patent No. 5759817
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
TITLE OF INVENTION: PHAGEMIDS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10550 No. 5759817th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,730A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bingham, Douglas A
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SCRF0707P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-784-2937

TELEFAX: 619-784-9399
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-322-730A-107

Query Match 4.3%; Score 18; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCCGCCAC 84
|||||
Db 31 ATGAGAGCCACCCGCCAC 14

RESULT 5

US-08-387-874-79/c
Sequence 79, Application US/08387874
Patent No. 5770356

GENERAL INFORMATION:

APPLICANT: Light, Paul L., II

APPLICANT: Lerner, Richard A.

TITLE OF INVENTION: PHAGEMIDS COEXPRESSING A SURFACE

TITLE OF INVENTION: RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN

NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10666 No. 5770356th Torrey Pines Road, Suite 220,

STREET: Mail Drop 1PC8

CITY: La Jolla

STATE: CA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,874

FILING DATE: 22-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: PCT/US93/08364

APPLICATION NUMBER: 03-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/941,369

FILING DATE: 04-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 303.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 79:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-387-874-79

Query Match 4.3%; Score 18; DB 1; Length 48;

Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCCGCCAC 84
|||||
Db 31 ATGAGAGCCACCCGCCAC 14

RESULT 6

US-08-899-575-35/c
Sequence 35, Application US/08899575
Patent No. 5770440

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R

APPLICANT: Barbas, Carlos F

APPLICANT: Lerner, Richard A

TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS

NUMBER OF SEQUENCES: 170

CORRESPONDENCE ADDRESS: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,

STREET: Mail Drop 1PC8

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/899,575

FILING DATE: 24-JUL-1997

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 08/276,852

APPLICATION NUMBER: 18-JUL-1994

FILING DATE: 30-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/954,148

FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SCR1452P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-899-575-35

Query Match 4.3%; Score 18; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCCGCCAC 84
|||||
Db 31 ATGAGAGCCACCCGCCAC 14

RESULT 7

US-08-899-575-35/C
Sequence 35, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-899-575-35

Query Match 4.3%; Score 18; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
DB 31 ATGAGAGCCACCGCCAC 14

RESULT 8
US-08-383-619-107/C
Sequence 107, Application US/08383619
Patent No. 5955341
GENERAL INFORMATION:
APPLICANT: Kang, Angray
APPLICANT: Barbas, Carlos
APPLICANT: Lerner, Richard
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
TITLE OF INVENTION: PHAGEMIDS

NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: DOUGLAS A. BINGHAM
STREET: 11300 Sorrento Valley Road, Suite 200
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,619
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,680
FILING DATE:
APPLICATION NUMBER: US/07/663,602
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bingham, Douglas A.
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SCR0371P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1555
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-383-619-107

Query Match 4.3%; Score 18; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
DB 31 ATGAGAGCCACCGCCAC 14

RESULT 9
US-08-888-366-36/C
Sequence 36, Application US/08888366
Patent No. 5972656
GENERAL INFORMATION:
APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwane E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-888-366-36

Query Match 4.3%; Score 18; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGGAGAGCCACCGCCAC 84
DB 31 ATGGAGAGCCACCGCCAC 14

RESULT 10
US-08-767-128-43/C
Sequence 43, Application US/08767128
Patent No. 611079
GENERAL INFORMATION:
APPLICANT: WYILE, Dwayne E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
NUMBER OF INVENTION: NUCLEOTIDES CODING THEREFORE
CORRESPONDENCE ADDRESS:
ADDRESS: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 611079west Center, 30 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSBQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-767-128-43

Query Match 4.3%; Score 18; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGGAGAGCCACCGCCAC 84
DB 31 ATGGAGAGCCACCGCCAC 14

RESULT 11
US-08-907-739-107/C
Sequence 107, Application US/08907739
Patent No. 6235469
GENERAL INFORMATION:
APPLICANT: Kang, Angrey
APPLICANT: Barbos, Carlos
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
NUMBER OF INVENTION: PHAGEIDS
CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of
STREET: 10666 No. 6235469th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,739
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/133,011
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-907-739-107

Query Match 4.3%; Score 18; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
DB 31 ATGAGAGCCACCGCCAC 14

RESULT 12
US-08-972-564-19/C
Sequence 19, Application US/08972564
Patent No. 6376170
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R.
APPLICANT: Burioni, Roberto
APPLICANT: Williams, R. Anthony
APPLICANT: Sanna, Pietro Paolo
TITLE OF INVENTION: LIGAND CAPTURE-DIRECTED SELECTION OF ANTIBODY
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Spensley Horn Juba & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,564
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/316,914
FILING DATE: October 3, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Hilde, Ph.D.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD-3809
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS

LOCATION: 1..48
US-08-972-564-19

Query Match 4.3%; Score 18; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
DB 31 ATGAGAGCCACCGCCAC 14

RESULT 13
US-09-729-597-107/C
Sequence 107, Application US/09729597
Patent No. 6468738
GENERAL INFORMATION:
APPLICANT: Kang, Angray
Barbas, Carlos
Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING PHAGEMIDS
NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
ADDRESSER: The Scripps Research Institute, Office of Patent Counsel
STREET: 10666 No. 6468738th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/729,597
FILING DATE: 04-Dec-2000
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/133,011
FILING DATE: 1994-09-29
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-09-729-597-107

Query Match 4.3%; Score 18; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
DB 31 ATGAGAGCCACCGCCAC 14

RESULT 14
PCT-US93-08364-79/c
Sequence 79, Application PC/TUS9308364
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PHAGMIDS COEXPRESSING A SURFACE
RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN
NUMBER OF SEQUENCES: 97
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08364
FILING DATE: 03-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,369
FILING DATE: 04-SEP-1992
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US93-08364-79

Query Match 4.3%; Score 18; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
|||
Db 31 ATGAGAGCCACCGCCAC 14

RESULT 15
PCT-US95-00067-21/c
Sequence 21, Application PC/TUS9500067
GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HERPES
TITLE OF INVENTION: SIMPLEX VIRUS AND METHODS THEREFOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00067
FILING DATE: 04-JAN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-3229
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..48
PCT-US95-00067-21

Query Match 4.3%; Score 18; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
|||
Db 31 ATGAGAGCCACCGCCAC 14

Search completed: March 22, 2004, 05:13:49
Job time : 84 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: March 22, 2004, 03:25:06 / Search time 311 Seconds
(without alignments)
4959.958 Million cell updates/sec

Title: US-10-032-159A-15

Perfect score: 417
Sequence: 1 atggggaactgtgcgcgag.....gctcctcgtgaaccacgagn 417

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2438257 seqs, 1849576744 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1556246

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	4.3	48	13	US-10-079-802-19
C 2	18	4.3	48	15	US-10-016-986-15
C 3	18	4.3	48	15	US-10-273-973-107
C 4	17	4.1	60	10	US-09-908-975-11168
C 5	16	3.8	22	14	US-10-321-195-12
C 6	15	3.6	17	14	US-10-238-700-3063
C 7	15	3.6	20	14	US-10-331-907-358
C 8	15	3.6	25	14	US-10-038-2638-98776
C 9	15	3.6	65	10	US-09-908-975-1082
C 10	15	3.6	65	10	US-09-908-975-28907
C 11	15	3.6	94	9	US-09-864-761-20254
C 12	14	3.4	17	14	US-10-238-700-3062
C 13	14	3.4	17	14	US-10-061-201-809
C 14	14	3.4	17	14	US-10-061-201-810
C 15	14	3.4	17	14	US-10-061-201-811

16	14	3.4	17	14	US-10-061-201-812	Sequence 812, App
C 17	14	3.4	18	14	US-10-181-603-14	Sequence 14, App1
C 18	14	3.4	20	10	US-09-953-611-85	Sequence 85, App1
C 19	14	3.4	20	15	US-10-349-143-55992	Sequence 5992, App
C 20	14	3.4	21	14	US-10-010-920-60	Sequence 60, App1
C 21	14	3.4	21	14	US-10-008-721-60	Sequence 60, App1
C 22	14	3.4	24	9	US-09-779-879A-29	Sequence 29, App1
C 23	14	3.4	24	9	US-09-779-880A-29	Sequence 29, App1
C 24	14	3.4	24	9	US-09-988-899-51	Sequence 51, App1
C 25	14	3.4	24	9	US-09-910-120-18	Sequence 18, App1
C 26	14	3.4	24	10	US-09-833-041-42	Sequence 42, App1
C 27	14	3.4	24	11	US-09-833-245-42	Sequence 42, App1
C 28	14	3.4	24	12	US-10-649-273-39	Sequence 39, App1
C 29	14	3.4	24	12	US-10-351-891-18	Sequence 18, App1
C 30	14	3.4	24	12	US-10-651-722-39	Sequence 39, App1
C 31	14	3.4	24	13	US-10-039-785-12	Sequence 12, App1
C 32	14	3.4	24	13	US-10-153-064-39	Sequence 39, App1
C 33	14	3.4	24	14	US-10-077-023-127	Sequence 127, App
C 34	14	3.4	24	14	US-10-075-846-44	Sequence 44, App1
C 35	14	3.4	24	14	US-10-056-884-37	Sequence 37, App1
C 36	14	3.4	24	14	US-10-080-980-34	Sequence 34, App1
C 37	14	3.4	24	14	US-10-092-135-44	Sequence 44, App1
C 38	14	3.4	24	14	US-10-086-185-64	Sequence 64, App1
C 39	14	3.4	24	14	US-10-081-775-34	Sequence 34, App1
C 40	14	3.4	24	14	US-10-067-443-39	Sequence 39, App1
C 41	14	3.4	24	14	US-10-104-943-100	Sequence 100, App1
C 42	14	3.4	24	14	US-10-120-604-146	Sequence 146, App
C 43	14	3.4	24	14	US-10-067-649-60	Sequence 60, App1
C 44	14	3.4	24	14	US-10-067-800-29	Sequence 29, App1
C 45	14	3.4	24	14	US-10-133-797-38	Sequence 38, App1

ALIGNMENTS

RESULT 1
US-10-079-802-19/C
Sequence 19, Application US/10079802
Publication No. US20020168629A1
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R.
Burton, Roberto
Williamson, R. Anthony
Sanna, Pietro Paolo
TITLE OF INVENTION: LIGAND CAPTURE-DIRECTED SELECTION OF ANTIBODY
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Spensley Horn Juba & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/079,802
FILING DATE: 19-Feb-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/316,914
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: LISA A. HALL, PH.D.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD-3809
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 19:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..48
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-079-802-19

Query Match 4.3%; Score 18; DB 13; Length 48;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
Db 31 ATGAGAGCCACCGCCAC 14

RESULT 2
US-10-016-986-35/c
; Sequence 35, Application US/10016986
; Publication No. US20030187247A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos F
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 313.2CON1
; CURRENT APPLICATION NUMBER: US/10/016,986
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 09/149,898
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 08/899,575
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 08/276,852
; PRIOR FILING DATE: 1994-07-18
; PRIOR APPLICATION NUMBER: US 08/178,302
; PRIOR FILING DATE: 1994-01-06
; PRIOR APPLICATION NUMBER: PCT/US93/09328
; PRIOR FILING DATE: 1993-09-30
; PRIOR APPLICATION NUMBER: US 07/954,148
; PRIOR FILING DATE: 1992-09-30
; NUMBER OF SEQ. ID NOS: 176
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
US-10-016-986-35

Query Match 4.3%; Score 18; DB 14; Length 48;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
Db 31 ATGAGAGCCACCGCCAC 14

RESULT 3
US-10-273-973-107/c
; Sequence 107, Application US/10273973
; Publication No. US20040002057A1
; GENERAL INFORMATION:
; APPLICANT: Kang, Angray
; APPLICANT: Barbas, Carlos
; APPLICANT: Lerner, Richard A.
```

```

;
; TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
; FRAGMENTIDS
; NUMBER OF SEQUENCES: 161
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; Patent Counsel
; STREET: 10666 No. US20040002057A1ch Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/273,973
; FILING DATE: 22-Jan-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,011
; FILING DATE: 08-JUN-1994
; APPLICATION NUMBER: US 07/683,602
; FILING DATE: 10-APR-1991
; APPLICATION NUMBER: US 07/826,623
; FILING DATE: 27-JAN-1992
; APPLICATION NUMBER: PCT/US 92/03091
; FILING DATE: 10-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitling, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: SCRF 238.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 107:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-10-273-973-107

Query Match 4.3%; Score 18; DB 15; Length 48;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
Db 31 ATGAGAGCCACCGCCAC 14

RESULT 4
US-09-908-975-11168
; Sequence 1168, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
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;; PRIOR FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: US 60/221,607
;; PRIOR FILING DATE: 2000-07-28
;; NUMBER OF SEQ ID NOS: 32337
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 11168
;; LENGTH: 60
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-908-975-11168

Query Match 4.1%; Score 17; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Gaps 0;

QY 390 GAACCTCAGGCTCTCTG 406
DB 37 GAACCTCAGGCTCTCTG 53

RESULT 5
US-10-321-195-12
;; Sequence 12, Application US/10321195
;; Publication No. US20030148353A1
;; GENERAL INFORMATION:
;; APPLICANT: Boirebaeck, Carl A.
;; APPLICANT: Malmberg-Hager, Ann-Christina
;; APPLICANT: Furebring, Christina
;; APPLICANT: Soderlund, Ulf H.
;; APPLICANT: Ottosson, Rebecca I.
;; TITLE OF INVENTION: A Method For In Vitro Molecular
;; FILE REFERENCE: 0046-P02150US1
;; CURRENT APPLICATION NUMBER: US/10/321,195
;; PRIOR FILING DATE: 2003-04-03
;; PRIOR APPLICATION NUMBER: 09/445,649
;; PRIOR FILING DATE: 2000-04-06
;; PRIOR APPLICATION NUMBER: PCT/GB98/01757
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: GB9712512.4
;; PRIOR FILING DATE: 1997-06-16
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 12
;; LENGTH: 22
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Primer
US-10-321-195-12

Query Match 3.8%; Score 16; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 GGAGAGCCACCGCCAC 84
DB 1 GGAGAGCCACCGCCAC 16

RESULT 6
US-10-238-700-3063
;; Sequence 3063, Application US/10238700
;; Publication No. US20030153521A1
;; GENERAL INFORMATION:
;; APPLICANT: Ribozyme Pharmaceuticals, Inc.
;; APPLICANT: McSwigen, James
;; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
;; FILE REFERENCE: 400/057 (MBH01-1158-A)
;; CURRENT APPLICATION NUMBER: US/10/238,700
;; CURRENT FILING DATE: 2002-09-18
;; PRIOR APPLICATION NUMBER: PCT/US 02/16840
;; PRIOR FILING DATE: 2002-05-29

;; PRIOR APPLICATION NUMBER: US 60/318,471
;; PRIOR FILING DATE: 2001-09-10
;; NUMBER OF SEQ ID NOS: 4666
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 3063
;; LENGTH: 17
;; TYPE: RNA
;; ORGANISM: Homo sapiens
US-10-238-700-3063

Query Match 3.6%; Score 15; DB 14; Length 17;
Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 194 ACAGCGCCATGCGCG 208
DB 1 ACAGCGCCATGCGCG 15

RESULT 7
US-10-331-907-358/C
;; Sequence 358, Application US/10331907
;; Publication No. US20030181660A1
;; GENERAL INFORMATION:
;; APPLICANT: Todd, John A.
;; Heess, John W
;; Caskey, Charles T
;; Cox, Roger D
;; Gerhold, David
;; Hammond, Holly
;; Hey, Patricia
;; Kawaguchi, Yoshihiko
;; Merriman, Tony R
;; Metzker, Michael L
;; TITLE OF INVENTION: No. US20030181660A1e1 LDL-Receptor
;; NUMBER OF SEQUENCES: 455
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Nixon and Vanderhye
;; STREET: 1100 No. US20030181660A1e1 Glebe Road, Eighth Floor
;; CITY: Arlington
;; STATE: Virginia
;; COUNTRY: US
;; ZIP: VA 22201-4714
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/331,907
;; FILING DATE: 31-Dec-2002
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/402,923A
;; FILING DATE: 14-Feb-2001
;; APPLICATION NUMBER: PCT/GB98/01102
;; FILING DATE: 15-APR-1998
;; APPLICATION NUMBER: US 60/043,553
;; FILING DATE: 15-APR-1997
;; APPLICATION NUMBER: US 60/048,740
;; FILING DATE: 05-JUN-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: B.V.Sadoff
;; REGISTRATION NUMBER: 36,663
;; REFERENCE/DOCKET NUMBER: 620-81
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4091
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 358:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 358;
US-10-331-907-358

Query Match 3.6%; Score 15; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 GGAGTGCTGCACAG 179
DB 20 GGAGTGCTGCACAG 6

RESULT 8
US-10-098-263B-98776

Sequence 98776, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miteam, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
PRIOR FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 98776
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-98776

Query Match 3.6%; Score 15; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 CTTCCTGGAGAGCCT 275
DB 9 CTTCCTGGAGAGCCT 23

RESULT 9
US-09-908-975-1082

Sequence 1082, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1082
LENGTH: 65
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-908-975-1082

Query Match 3.6%; Score 15; DB 10; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 ACGCTGATCTGCC 107

DB 11 ACGCTGATCTGCC 25

RESULT 10
US-09-908-975-28907

Sequence 28907, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 28907
LENGTH: 65
TYPE: DNA
ORGANISM: Mus musculus
US-09-908-975-28907

Query Match 3.6%; Score 15; DB 10; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 270 GAGCTGAAGTTCCA 284
DB 26 GAGCTGAAGTTCCA 40

RESULT 11
US-09-864-761-20254

Sequence 20254, Application US/03864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecolica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Autonomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20254
LENGTH: 94
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007097.2
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: NT HIT: AB011536.1, EVALUATE 6.60e-01
OTHER INFORMATION: EST_HUMAN HIT: BE677194.1, EVALUATE 5.00e-46
US-09-864-761-20254

Query Match 3.6%; Score 15; DB 9; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 GTGCTGGCCGCGTG 156
DB 49 GTGCTGGCCGCGTG 63

RESULT 12
US-10-238-700-3062
Sequence 3062, Application US/10238700
Publication No. US20030153521A1
GENERAL INFORMATION:
APPLICANT: McSwigen, James
TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
FILE REFERENCE: 400/057 (MHB01-1158-A)
CURRENT APPLICATION NUMBER: US/10/238,700
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: PCT/US 02/16840
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US 60/318,471
PRIOR FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 4666
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3062
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-238-700-3062

Query Match 3.4%; Score 14; DB 14; Length 17;
Best Local Similarity 92.9%; Pred. No. 5.4e+03;

Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 194 ACAGCCGCGATGCGG 207
DB 4 ACAGCCGCGATGCGG 17

RESULT 13
US-10-061-201-809
Sequence 809, Application US/10061201
Publication No. US20030166229A1
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
PRIOR FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/328,205
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 809
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-10-061-201-809

Query Match 3.4%; Score 14; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 CTGCCCCAGCCGCC 115
DB 4 CTGCCCCAGCCGCC 17

RESULT 14
US-10-061-201-810
Sequence 810, Application US/10061201
Publication No. US20030166229A1
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178
CURRENT APPLICATION NUMBER: US/10/061,201
PRIOR FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
US-10-061-201-810

Search completed: March 22, 2004, 05:19:21
Job time : 322 secs

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/328,205
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 810
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-10-061-201-810

Query Match 3.4%; Score 14; DB 14; Length 17;
Best Local Similarity 100.0%; Pred.No. 5.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 CTGCCCGAGCGCC 115
DB 3 CTGCCCGAGCGCC 16

RESULT 15
US-10-061-201-811
Sequence 811, Application US/10061201
Publication No. US20030166229A1
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
FILE REFERENCE: PB0178
CURRENT APPLICATION NUMBER: US//10/061,201
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/328,205
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 4162
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 811
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-10-061-201-811

Query Match 3.4%; Score 14; DB 14; Length 17;
Best Local Similarity 100.0%; Pred.No. 5.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 CTGCCCGAGCGCC 115
DB 2 CTGCCCGAGCGCC 15

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 03:19:00 ; Search time 3013 Seconds
(without alignments)
4132.934 Million cell updates/sec

Title: US-10-032-159a-15

Perfect score: 417
Sequence: 1 atgggggagactgtgcgcag.....ggtccctcgtgtaaccacagm 417

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 569298

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estropl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_est1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	16	3.8	65	CD949815 SAN_244 G
2	16	3.8	87	BF180861
3	15	3.6	62	AT739447
4	15	3.6	70	AA629219

5	15	3.6	76	AI138663
6	15	3.6	79	AA731299
7	15	3.6	79	AA877223
8	15	3.6	81	BH220418
9	15	3.6	85	AI605313
10	15	3.6	91	BQ758392
11	15	3.6	100	AA510788
12	15	3.6	100	BF110926
13	15	3.6	100	AA502296
14	15	3.4	37	AZ771602
15	14	3.4	43	AI014286
16	14	3.4	48	AZ786204
17	14	3.4	43	AI358130
18	14	3.4	50	AI05866
19	14	3.4	50	AI06959
20	14	3.4	50	AI06972
21	14	3.4	50	AI06973
22	14	3.4	50	AI06974
23	14	3.4	50	AI06976
24	14	3.4	50	AI06977
25	14	3.4	50	AI06978
26	14	3.4	56	AZ801785
27	14	3.4	57	CG733686
28	14	3.4	60	CNS0290X
29	14	3.4	71	AI990431
30	14	3.4	73	AI990431
31	14	3.4	75	BE737572
32	14	3.4	75	CG709037
33	14	3.4	78	AI628233
34	14	3.4	81	AZ919233
35	14	3.4	81	CG733644
36	14	3.4	82	CG710246
37	14	3.4	84	N89309
38	14	3.4	84	CG721982
39	14	3.4	88	AA172789
40	14	3.4	90	CG733649
41	14	3.4	92	BF591436
42	14	3.4	92	BZ592694
43	14	3.4	93	CG709055
44	14	3.4	92	CG712696
45	14	3.4	97	BF148426

ALIGNMENTS

RESULT 1
CD949815/c 65 bp mRNA linear EST 15-JUL-2003
LOCUS SAN_244 GenetAg2 Zea mays cDNA, mRNA sequence.
DEFINITION CD949815
ACCESSION CD949815
VERSION CD949815.1 GI:32797575
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Cistaceae; Panicoideae; Andropogoneae; Zea.
EST.
1 (bases 1 to 65)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (2003)
Contact: Genopiante
Genopiante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genopiante' (http://www.genopiante.com
and http://genopiante-info.inbioigen.fr).

FEATURES
source
1..65
/organism="Zea mays"

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ORIGIN
Query Match      3.8%; Score 16; DB 14; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
385 TCTAGGAACCTCAGGC 400
|||||
22 TCTAGGAACCTCAGGC 7

DB
22 TCTAGGAACCTCAGGC 7

RESULT 2
LOCUS      BF180861
DEFINITION 601804988B1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4036077 5',
ACCESSION  BF180861
VERSION     BF180861.1 GI:11059003
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 87)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
           DNA sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LNL at:
           http://image.llnl.gov
           Plate: LAM9310 row: 0 column: 22
           High quality sequence stop: 87.
           Location/Qualifiers
             1..87
             /organism="Mus musculus"
             /mol_type="mRNA"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="IMAGE:4036077"
             /issue_type="tumor, gross tissue"
             /dev_stage="7 months"
             /lab_host="DH10B"
             /clone_1lb="NCI_CGAP_Mam5"
             /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
             Site 2: NciI; Cloned unidirectionally. Primer: Oligo dr.
             Library constructed by Life Technologies. Investigators
             providing samples: Lothar Hennighausen/Robin Humphreys,
             NIH"

ORIGIN
Query Match      3.8%; Score 16; DB 10; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
249 CGGGGCGATCGCCTTC 264
|||||
57 CGGGGCGATCGCCTTC 72

DB
57 CGGGGCGATCGCCTTC 72

RESULT 3
LOCUS      A1739447
DEFINITION 62 bp mRNA linear EST 20-DEC-1999
           w113f01.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2390137 3',

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ORIGIN
Query Match      3.6%; Score 15; DB 9; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
263 TCCTGGAGAGCCTGA 277
|||||
21 TCCTGGAGAGCCTGA 35

DB
21 TCCTGGAGAGCCTGA 35

RESULT 4
LOCUS      AA629219/c
DEFINITION 70 bp mRNA linear EST 16-OCT-1997
           zu73f07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743653
           3' similar to TR:G609419 G609419 CHROMOSOME XII COSMID 8039. ?;
           mRNA sequence.
           AA629219
           AA629219.1 GI:2541606
           EST.
           SOURCE     Homo sapiens (human)
           ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
           Reference   1 (bases 1 to 70)
           AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
           Krizman,D., Kucada,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
           Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
           Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
           WashU-NCI human EST Project

ORIGIN
Query Match      3.6%; Score 15; DB 9; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
263 TCCTGGAGAGCCTGA 277
|||||
21 TCCTGGAGAGCCTGA 35

DB
21 TCCTGGAGAGCCTGA 35

RESULT 4
LOCUS      AA629219/c
DEFINITION 70 bp mRNA linear EST 16-OCT-1997
           zu73f07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743653
           3' similar to TR:G609419 G609419 CHROMOSOME XII COSMID 8039. ?;
           mRNA sequence.
           AA629219
           AA629219.1 GI:2541606
           EST.
           SOURCE     Homo sapiens (human)
           ORGANISM   Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
           Reference   1 (bases 1 to 70)
           AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
           Krizman,D., Kucada,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
           Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
           Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
           WashU-NCI human EST Project

```

JOURNAL COMMENT

Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40m3 fwd. RT from Amersham
High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers

1..70

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:5930947"

/db_xref="taxon:9606"

/clone="IMAGE:743653"

/sex="male"

/lab_host="DH10B"

/clone_lib="Soares testis_NHT"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer 15'.

TTTACCATCTGAAAGTGGAGCGGCCCAATTTTCTTTTCTT 3'.

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 3.6%; Score 15; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 TTCTGTGAGAGCGCTG 276

Db 60 TTCTGTGAGAGCGCTG 46

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FEATURES

source

Insert Length: 170 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.

Location/Qualifiers

1..76

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2050363"

/tissue_type="stem cell 34+/38+"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="NCI CGAP HSC2"

/note="Organ: bone marrow; Vector: pAMP; mRNA made from bone marrow, stem cells 34+/38+, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 400 bp. Primary library, non-amplified."

ORIGIN

Query Match 3.6%; Score 15; DB 9; Length 76;
Best Local Similarity 100.0%; Pred. No. 3.3e+04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 142 GTGCTGTGCCAGCTG 156

Db 36 GTGCTGTGCCAGCTG 50

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AI1318663 76 bp mRNA linear EST 18-MAR-1998
ta80b10.x1 NCI CGAP HSC2 Homo sapiens cDNA clone IMAGE:2050363 3'
similar to TR:Q14489 Q14489 RIBOSOMAL PROTEIN S10; mRNA sequence.
AI1318663
AI1318663.1 GI:4034598
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 76)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: David B. Kitzman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbtp/image/image.html

Trace considered overall poor quality

AA731299 79 bp mRNA linear EST 07-FEB-1998
hw68g05.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1251800 3'
similar to TR:Q13425 Q13425 BETA2-SYNTROPHIN; mRNA sequence.
AA731299
AA731299.1 GI:2752503
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 79)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: Louis M. Staedt, M.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbtp/image/image.html

Trace considered overall poor quality

Insert Length: 1095 Std Error: 0.00
Seq primer: -40m3 fwd. RT from Amersham
High quality sequence stop: 1.

Location/Qualifiers

1..79

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1251800"

/tissue_type="germinal center B cell"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="NCI CGAP GCB1"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA

IMAGE:1038965 3', mRNA sequence.
 ACCESSION A1605313
 VERSION A1605313.1 GI:4614480
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 85)
 Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Ritzer,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watsn.wustl.edu
 This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:578989
 This clone was previously sequenced on the 5' end only, this new data is from the 3' end.
 Location/Qualifiers
 1..85
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="NIH SWISS"
 /db_xref="taxon:10090"
 /clone="IMAGE:1038965"
 /sex="pooled"
 /tissue_type="heart"
 /dev_stage="13 day embryos"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse heart (#937316)"
 /note="Organ: heart; Vector: pBluescript SK-; Site 1: EcoRI, Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGACG 3' ~3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'".
 ORIGIN
 Query Match 3.6%; Score 15; DB 9; Length 85;
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 211 GGGCAGCTTGCCTGANT 225
 |||||
 |||||
 Db 37 GGGCAGCTTGCCTGANT 23
 RESULT 10
 LOCUS BQ758392
 DEFINITION Hordeum vulgare subsp. vulgare cDNA clone EBma05_SQ001_108 5', mRNA sequence.
 ACCESSION BQ758392
 VERSION BQ758392.1 GI:21966864
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
 1 (bases 1 to 91)
 Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L., Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.

TITLE Development of Barley Transcriptome Resources
 JOURNAL Unpublished (2001)
 COMMENT Contact: Waugh R, Marshall D F
 Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: estecr@scrt.ac.uk.
 Location/Qualifiers
 1..91
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Optic"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="EBma05_SQ001_108"
 /tissue_type="maternal"
 /dev_stage="12 DPA"
 /lab_host="DH10B"
 /clone_lib="maternal, 12 DPA, no treatment, cv Optic, EBma05"
 /note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from maternal tissue dissected from developing grains (12 days post anthesis) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BSRG/SBRAD funded cereal 1GF (Investigating Gene Function) project."
 ORIGIN
 Query Match 3.6%; Score 15; DB 13; Length 91;
 Best Local Similarity 100.0%; Pred. No. 3.5e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 160 GAGGAGGAGCTGCTG 174
 |||||
 |||||
 Db 38 GAGGAGGAGCTGCTG 52
 RESULT 11
 LOCUS AA510788
 DEFINITION Vg31h04.r1 Soares mammary_gland_MOMG Mus musculus cDNA clone
 IMAGE:863191 5', mRNA sequence.
 ACCESSION AA510788
 VERSION AA510788.1 GI:2248642
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 100)
 Marra,M., Hillier,L., Allen,M., Bowers,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watsn.wustl.edu
 This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:507279
 Seg primer: -28m3 rev2 ET from Amerham
 High quality sequence stop: 84.
 Location/Qualifiers

FEATURES

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.6%; Score 15; DB 28; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 GGACGAGGAGAGGT 170
DB 73 GGACGAGGAGAGGT 87

RESULT 14 37 bp DNA linear GSS 16-FEB-2001
AZ771602
LOCUS 1M0573A17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0573A17 R, genomic survey sequence.
ACCESSION AZ771602
VERSION AZ771602.1 GI:12893864
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 37) Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, W., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0573 row: A column: 17

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 37.

Location/Qualifiers

FEATURES

source

1. 37
/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0573A17"

/sex="male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/shares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 3.4%; Score 14; DB 28; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 AGGTGCTGCACAGC 180
DB 9 AGGTGCTGCACAGC 22

RESULT 15 43 bp RNA linear EST 15-JUN-1998
A1014286
LOCUS 1M46602.1 Johnston frontal cortex Homo sapiens cDNA clone
DEFINITION IMAGE:1538570 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION
(HUMAN); mRNA sequence.
ACCESSION A1014286
VERSION A1014286.1 GI:3228118
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 43) Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Miller, J., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Maria, K.,
Martin, J., Moore, B., Scheinberg, R., Steptoe, M., Tan, F.,
Treising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

TITLE Washu-NCI human EST Project

Unpublished (1997)

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -40m13 fwd. RT from Amersham

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

1. 43
/organism="Homo sapiens"

/mol_type="RNA"

/db_xref="taxon:9606"

/clone="IMAGE:1538570"

/sex="male"

/tissue_type="pooled frontal lobe"

/dev_stage="adult"

/lab_host="SOLR (kanamycin resistant)"

/clone_lib="Johnston frontal cortex"

/note="Organ: Brain; Vector: Bluescript SK-; Site: 1;
ECORI; Stanley Neuropathology Consortium
(www.stanleylab.org) brains S-58, S-65, S-67, S-78.
Random + oligo-dT primed into EcoRI site of Zap II Vector.
Mass excised. Avg insert length 1.9kb. Custom library
provided by Dr. Nancy Johnston [(410) 614-3918,
nlj@wustl.edu].

ORIGIN

Query Match 3.4%; Score 14; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 8.5e+04;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 300 CACCTGTGTCACCG 313
| | | | | | | | | |
Db 21 CACCTGTGTCACCG 34

Search completed: March 22, 2004, 05:12:28
Job time : 3031 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 03:12:56 ; Search time 3050 Seconds

(without alignments)
5925.916 Million cell updates/sec

Title: US-10-032-159A-15

Perfect score: 417
Sequence: 1 atgggggagactgctgcgcag.....gctcctcgtgacccagm 417

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1846492

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sgs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_pl:*
25: em_pl:*
26: em_ro:*
27: em_sgs:*
28: em_un:*
29: em_vl:*
30: em_hg_hum:*
31: em_hg_inv:*
32: em_hg_other:*
33: em_hg_mus:*
34: em_hg_pln:*
35: em_hg_rnd:*
36: em_hg_mam:*
37: em_hg_vrt:*
38: em_sy:*
39: em_hggo_hum:*
40: em_hggo_mus:*
41: em_hggo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	18	4.3	39	6	A46185	A46185 Sequence 23
C 2	18	4.3	39	6	AR351110	AR351110 Sequence
C 3	18	4.3	48	6	AR038280	AR038280 Sequence
C 4	18	4.3	48	6	AR075276	AR075276 Sequence
C 5	18	4.3	48	6	AR081918	AR081918 Sequence
C 6	18	4.3	48	6	AR108691	AR108691 Sequence
C 7	18	4.3	48	6	AR152686	AR152686 Sequence
C 8	18	4.3	48	6	IS8569	IS8569 Sequence 35
C 9	18	4.3	48	6	IS1300	IS1300 Sequence 10
C 10	18	4.3	48	6	AR238528	AR238528 Sequence
C 11	18	4.3	48	6	AR357623	AR357623 Sequence
C 12	18	4.3	48	6	AX323341	AX323341 Sequence
C 13	17	4.1	66	6	E29068	E29068 Modified in
C 14	16	3.8	22	6	A81881	A81881 Sequence 12
C 15	16	3.8	22	6	AR120684	AR120684 Sequence
C 16	16	3.8	22	6	AR266660	AR266660 Sequence
C 17	16	3.8	22	6	BD135550	BD135550 A method
C 18	16	3.8	81	9	HSXTCRA07	X83782 H.sapiens m
C 19	15	3.6	20	6	A91597	A91597 Sequence 12
C 20	15	3.6	20	6	AR163855	AR163855 Sequence
C 21	15	3.6	20	6	AR305404	AR305404 Sequence
C 22	15	3.6	20	6	AR309508	AR309508 Sequence
C 23	15	3.6	20	6	BD023379	BD023379 Method fo
C 24	15	3.6	20	6	BD106315	BD106315 Novel LDL
C 25	15	3.6	29	6	BD187047	BD187047 Polypepti
C 26	15	3.6	42	6	AR336828	AR336828 Sequence
C 27	15	3.6	42	6	AR336829	AR336829 Sequence
C 28	15	3.6	42	9	HSAL10886	AJ010886 Homo sapi
C 29	15	3.6	71	6	AR316846	AR316846 Sequence
C 30	15	3.6	71	6	AR336826	AR336826 Sequence
C 31	15	3.6	71	6	AX039943	AX039943 Sequence
C 32	15	3.6	74	11	AB091414	AB091414 Sus scrofa
C 33	15	3.6	82	10	RNO230619	AJ230619 Rattus no
C 34	15	3.6	99	6	AX023606	AX023606 Sequence
C 35	15	3.4	17	6	AX531300	AX531300 Sequence
C 36	14	3.4	17	6	AX531301	AX531301 Sequence
C 37	14	3.4	17	6	AX531302	AX531302 Sequence
C 38	14	3.4	17	6	AX531303	AX531303 Sequence
C 39	14	3.4	18	6	AR054201	AR054201 Sequence
C 40	14	3.4	18	6	AR087097	AR087097 Sequence
C 41	14	3.4	18	6	AR121118	AR121118 Sequence
C 42	14	3.4	18	6	AX754814	AX754814 Sequence
C 43	14	3.4	18	6	AX754824	AX754824 Sequence
C 44	14	3.4	18	6	AX754837	AX754837 Sequence
C 45	14	3.4	20	6	AR294257	AR294257 Sequence

ALIGNMENTS

RESULT 1
A46185/c
LOCUS A46185
DEFINITION Sequence 23 from Patent WO951914.
ACCESSION A46185
VERSION A46185.1 GI:2300433
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 39)
AUTHORS Sodoyer, R., Aujame, L. and Geoffroy, F.
TITLE METHOD FOR PREPARING A MULTICOMBINATORIAL LIBRARY OF ANTIBODY GENE
EXPRESSION VECTORS
JOURNAL Patent: WO 9521914-A 23 17-AUG-1995;

COMMENT PASTEUR MERIEUX SERUMS VACC (FR)
Other publication RU 166895 950829
Other publication FR 2715940 950811.
FEATURES
source 1. .39
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 4.3%; Score 18; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 ATGGAGAGCCACCGCCAC 84
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27 ATGGAGAGCCACCGCCAC 10

RESULT 2
AR361110/c AR361110 39 bp DNA linear PAT 17-AUG-2003
LOCUS AR361110
DEFINITION Sequence 23 from patent US 6595697.
ACCESSION AR361110
VERSION AR361110.1 GI:33768813
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 39)
AUTHORS Sodoyer, R., Aujame, L. and Geoffroy, F.
TITLE Process for preparing a multicombinatorial library of vectors for
expressing antibody genes
JOURNAL Patent: US 6595697-A 23 29-JUL-2003;
FEATURES
source 1. .39
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 4.3%; Score 18; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 ATGGAGAGCCACCGCCAC 84
|||||
27 ATGGAGAGCCACCGCCAC 10

RESULT 3
AR038280/c AR038280 48 bp DNA linear PAT 29-SEP-1999
LOCUS AR038280
DEFINITION Sequence 35 from patent US 5804440.
ACCESSION AR038280
VERSION AR038280.1 GI:5956997
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 48)
AUTHORS Burton, D.R., Barbas, C.F. and Lerner, R.A.
TITLE Human neutralizing monoclonal antibodies to human immunodeficiency
virus
JOURNAL Patent: US 5804440-A 35 08-SEP-1999;
FEATURES
source 1. .48
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 4.3%; Score 18; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 ATGGAGAGCCACCGCCAC 84
|||||
Db 31 ATGGAGAGCCACCGCCAC 14

RESULT 4
AR075276/c AR075276 48 bp DNA linear PAT 28-AUG-2000
LOCUS AR075276
DEFINITION Sequence 107 from patent US 5955341.
ACCESSION AR075276
VERSION AR075276.1 GI:10002027
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 48)
AUTHORS Kang, A., Barbas, C. and Lerner, R.
TITLE Heterodimeric receptor libraries using phagemids
JOURNAL Patent: US 5955341-A 107 21-SEP-1999;
FEATURES
source 1. .48
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 4.3%; Score 18; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 ATGGAGAGCCACCGCCAC 84
|||||
Db 31 ATGGAGAGCCACCGCCAC 14

RESULT 5
AR081918/c AR081918 48 bp DNA linear PAT 31-AUG-2000
LOCUS AR081918
DEFINITION Sequence 36 from patent US 5972656.
ACCESSION AR081918
VERSION AR081918.1 GI:10008644
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 48)
AUTHORS Lopez, O., Wylie, D.E. and Wagner, F.W.
TITLE Mercury binding polypeptides and nucleotides coding therefore
JOURNAL Patent: US 5972656-A 36 26-OCT-1999;
FEATURES
source 1. .48
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 4.3%; Score 18; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 ATGGAGAGCCACCGCCAC 84
|||||
Db 31 ATGGAGAGCCACCGCCAC 14

RESULT 6
AR108691/c AR108691 48 bp DNA linear PAT 14-FEB-2001
LOCUS AR108691
DEFINITION Sequence 43 from patent US 611079.
ACCESSION AR108691
VERSION AR108691.1 GI:12824178
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 48)
AUTHORS Wylie,D.E., Lopez,O., Murray,P.,Joseph, and Goebel,P.
TITLE Lead binding polypeptides and nucleotides coding therefore
JOURNAL Patent: US 6111079-A 43 29-AUG-2000;
FEATURES Location/Qualifiers

SOURCE

1..48
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 4.3%; Score 18; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
Db 31 ATGAGAGCCACCGCCAC 14

RESULT 7

AR152688/c AR152688 48 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 107 from patent US 6235469.
DEFINITION AR152688
ACCESSION AR152688
VERSION AR152688.1 GI:15120220
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 48)
AUTHORS Kang,A., Barbas,C. and Lerner,R.A.
TITLE Heterodimeric receptor libraries using phagemids
JOURNAL Patent: US 6235469-A 107 22-MAY-2001;
FEATURES Location/Qualifiers

SOURCE

1..48
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 4.3%; Score 18; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
Db 31 ATGAGAGCCACCGCCAC 14

RESULT 8

158569/c 158569 48 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 35 from patent US 5652138.
DEFINITION 158569
ACCESSION 158569
VERSION 158569.1 GI:2477807
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 48)
AUTHORS Burton,D.R., Barbas,C.F. and Lerner,R.A.
TITLE Human neutralizing monoclonal antibodies to human immunodeficiency virus
JOURNAL Patent: US 5652138-A 35 29-JUL-1997;
FEATURES Location/Qualifiers

SOURCE

1..48
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 4.3%; Score 18; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
Db 31 ATGAGAGCCACCGCCAC 14

RESULT 9
161300/c 161300 48 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 107 from patent US 5658727.
DEFINITION 161300
ACCESSION 161300
VERSION 161300.1 GI:2479248
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 48)
AUTHORS Barbas,C., Kang,A. and Lerner,R.A.
TITLE Heterodimeric receptor libraries using phagemids
JOURNAL Patent: US 5658727-A 107 19-AUG-1997;
FEATURES Location/Qualifiers

SOURCE

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/mol_type="unassigned DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
Db 31 ATGAGAGCCACCGCCAC 14

RESULT 10
AR238528/c AR238528 48 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 107 from patent US 6468738.
DEFINITION AR238528
ACCESSION AR238528
VERSION AR238528.1 GI:27283526
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 48)
AUTHORS Kang,A., Barbas,C. and Lerner,R.A.
TITLE Heterodimeric receptor libraries using phagemids
JOURNAL Patent: US 6468738-A 107 22-OCT-2002;
FEATURES Location/Qualifiers

SOURCE

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/organism="unknown"
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ORIGIN

Query Match 4.3%; Score 18; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
Db 31 ATGAGAGCCACCGCCAC 14

RESULT 11
AR367623/c AR367623 48 bp DNA linear PAT 12-SEP-2003
LOCUS Sequence 19 from patent US 6376170.
DEFINITION AR367623
ACCESSION AR367623
VERSION AR367623.1 GI:34600987
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
 1 (bases 1 to 48)
 REFERENCE Burton,D.R., Burton,R., Williamson,R.A. and Sanna,P.P.
 AUTHORS
 TITLE Ligand capture-directed selection of antibody
 JOURNAL Patent: US 6376170-A 19 23-APR-2002;
 FEATURES Location/Qualifiers
 source 1..48
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Query Match 4.3%; Score 18; DB 6; Length 48;
 Best Local Similarity 100.0%; Pred.No. 8.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
 |||||
 DB 31 ATGAGAGCCACCGCCAC 14

RESULT 12
 AX323341/c 48 bp DNA linear PAT 07-JAN-2002
 LOCUS
 DEFINITION Sequence 79 from Patent EP162270.
 ACCESSION AX323341
 VERSION AX323341.1 GI:18094102
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1
 .AUTHORS Light,J.P. and Lerner,R.A.
 TITLE Phagemids coexpressing a surface receptor and a surface
 heterologous protein
 JOURNAL Patent: EP 1162270-A 79 12-DEC-2001;
 FEATURES THE SCRIPPS RESEARCH INSTITUTE (US)
 source Location/Qualifiers
 1..48
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 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"
 /note="synthesized"

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 Best Local Similarity 100.0%; Pred.No. 8.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
 |||||
 DB 31 ATGAGAGCCACCGCCAC 14

RESULT 13
 E29068 66 bp DNA linear PAT 18-JUN-2001
 LOCUS
 DEFINITION Modified interferon tau-3.
 ACCESSION E29068
 VERSION E29068.1 GI:13025516
 KEYWORDS JP 1999042089-A/3.
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 66)
 .AUTHORS Masako,I. and Takashi,N.
 TITLE Modified interferon tau-3
 JOURNAL Patent: JP 1999042089-A 3 16-FEB-1999;
 COMMENT OS Unidentified
 PN JP 1999042089-A/3
 PD 16-FEB-1999
 PR 29-JUL-1997 JP 1997203137

PI MASANO ISHIMURA, TAKASHI NISHIGAKI
 PC C12N15/09,A61K38/21,C07K14/555,C12N1/21,C12P21/02//
 PC (C12N15/09,C12R1:91), (C12P21/02,C1R1:19), C12N15/00,A61K37/66,
 PC (C12N15/00,C12R1:91)
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key
 FT source 1..66
 /organism="Unidentified".
 FEATURES Location/Qualifiers
 source 1..66
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

ORIGIN
 Query Match 4.1%; Score 17; DB 6; Length 66;
 Best Local Similarity 100.0%; Pred.No. 2.8e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 GAACCTCAGGCTCCTGG 406
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 DB 42 GAACCTCAGGCTCCTGG 58

RESULT 14
 A81881 22 bp DNA linear PAT 21-JAN-2000
 LOCUS
 DEFINITION Sequence 12 from Patent WO9858080.
 ACCESSION A81881
 VERSION A81881.1 GI:6731895
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 22)
 .AUTHORS Soederlind,U.H. and Borrebaeck,C.A.
 TITLE A METHOD FOR IN VITRO MOLECULAR EVOLUTION OF PROTEIN FUNCTION
 JOURNAL Patent: WO 9858080-A 12 23-DEC-1998;
 FEATURES CRIPPS JOHANNA ELIZABETH (GB); SOEDERLIND ULF HANS ESKIL (SE)
 source Location/Qualifiers
 1..22
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

ORIGIN
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 Best Local Similarity 100.0%; Pred.No. 1e+04;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 GGAGAGCCACCGCCAC 84
 |||||
 DB 1 GGAGAGCCACCGCCAC 16

RESULT 15
 AR120684 22 bp DNA linear PAT 16-MAY-2001
 LOCUS
 DEFINITION Sequence 12 from patent US 6159690.
 ACCESSION AR120684
 VERSION AR120684.1 GI:14104260
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 22)
 .AUTHORS Borrebaeck,C.Arne,Krister., Soederlind,U.Hans,Eskil. and
 Ottosson,R.Ingrid,Camilla.
 TITLE Method for in vitro molecular evolution of protein function using
 exonuclease and amplification
 JOURNAL Patent: US 6159690-A 12 12-DEC-2000;
 FEATURES Location/Qualifiers

source

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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 GGAGAGCCACCGCCAC 84
|||||||
Db 1 GGAGAGCCACCGCCAC 16

Search completed: March 22, 2004, 04:21:44
Job time : 3056 secs

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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 02:19:50 ; Search time 391 Seconds
(without alignments)
4530.687 Million cell updates/sec

Title: US-10-032-159A-15

Perfect score: 417
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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 337863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3485926

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18	4.3	33	2	AAQ44650 PCR prime
C 2	18	4.3	39	2	AAQ95082 Multicom
C 3	18	4.3	48	2	AAQ78813 Membrane
C 4	18	4.3	48	2	AAQ64423 PCR prime
C 5	18	4.3	48	2	AAQ94730 cpiII mem
C 6	18	4.3	48	2	AAQ40878 pcomb2-3
C 7	18	4.3	48	2	AAQ58272 M13mp18 P
C 8	18	4.3	48	2	AAQ32124 Primer G-
C 9	18	4.3	48	3	AAQ30998 Primer G-
C 10	18	4.3	48	6	AAQ38725 cpiII mem
C 11	18	4.3	48	8	ADB84272 Dielsidero
C 12	17	4.1	60	6	ADB38420 Human spl
C 13	17	4.1	66	2	AAQ18458 PCR prime
C 14	15	3.6	17	7	ABZ61630 Human H-R
C 15	15	3.6	20	2	AAV85968 Mouse IRP
C 16	15	3.6	20	6	AAV41022 Primer CB
C 17	15	3.6	20	6	AB194287 Human C/E
C 18	15	3.6	25	8	ACT98785 Human m1c
C 19	15	3.6	29	7	ABZ71170 Human HIF
C 20	15	3.6	42	3	AAQ68563 TMOP svnt
C 21	15	3.6	42	9	ADQ35520 Trypsin m
C 22	15	3.6	42	9	ADQ35521 Trypsin m
C 23	15	3.6	43	3	AAQ65007 Human CTL

24	15	3.6	44	3	AAQ65006 Human CTL
C 25	15	3.6	52	3	AAQ65011 Human CTL
26	15	3.6	53	3	AAQ65010 Human CTL
27	15	3.6	65	6	ABN28334 Rat sPLIC
28	15	3.6	65	6	ABN56159 Mouse spl
29	15	3.6	71	3	AAQ68566 Green flu
30	15	3.6	71	9	ADQ35465 Pesticiida
C 31	15	3.6	77	2	AAQ45452 Sense str
32	15	3.6	94	4	AAI22793 Probe #12
33	15	3.6	94	4	ABA67880 Human fce
34	15	3.6	94	4	AAI48095 Probe #16
35	15	3.6	94	4	ABA49961 Human bre
36	15	3.6	94	4	ABA34934 Probe #13
37	15	3.6	94	4	AAK42028 Human bon
38	15	3.6	94	4	AAK16284 Human bra
39	15	3.6	94	4	ABS41637 Human liv
40	15	3.6	94	5	AAI08467 Probe #84
41	15	3.6	94	6	ABS16062 Human gen
42	15	3.6	99	3	AAA36687 RSV and P
C 43	14	3.4	17	6	ABV90099 Human POS
44	14	3.4	17	6	ABV90097 Human POS
45	14	3.4	17	6	ABV90098 Human POS

ALIGNMENTS

RESULT 1
ID AAQ44650 standard; DNA; 33 BP.
XX AAQ44650;
AC 25-MAR-2003 (revised)
DT 04-OCT-1994 (first entry)
XX PCR primer for amplifying mature cpiII membrane anchor gene.
DE Expression; insertion sequence; expression vector; hybrid;
KW filamentous phage; Rd; bacteriophage; cpiIII; membrane anchor; ss.
XX Synthetic.
XX OS WO9405781-A1.
XX EN
XX 17-MAR-1994.
XX PF 03-SEP-1993; 93MO-US008364.
XX PR 04-SEP-1992; 92US-00941369.
XX PA (SCRI) SCRIPPS RES INST.
XX PI Light JP, Lerner RA;
XX WP; 1994-101186/12.
XX PT Filamentous phage comprising a heterologous polypeptide and a
PT hetero: dimer - is used to detect the presence of a preselected ligand in
a sample.
XX PS Example 2g; Page 123; 232pp; English.
XX CC Two primers (AAQ44650, AAQ44651) were used to amplify the cpiII membrane
CC anchor domain using the replicative form of M13mp18 as a template
CC molecule for PCR. The primers also incorporated two restriction enzyme
CC recognition sites (SpeI and NheI) into the amplified molecule. (Updated
CC on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 33 BP; 5 A; 8 C; 12 G; 8 T; 0 U; 0 Other;
Query Match 4.3%; Score 18; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
 |||||
 Db 31 ATGAGAGCCACCGCCAC 14

RESULT 2
 AAQ95082/c
 ID AAQ95082 standard; DNA; 39 BP.
 XX
 AC AAQ95082;
 XX
 DT 19-MAR-1996 (first entry)
 XX
 DE Multicombinatorial vector library primer pVH GIII*.
 XX
 KM Multicombinatorial library; expression vector; antibody; recombination;
 KM light chain; heavy chain; variable region; pACYC177; lac promoter; attP;
 KM kanamycin resistance; origin of replication; pBluescript; pBR328; attB;
 KM peltB signal sequence; chloramphenicol resistance; ampicillin resistance;
 KM ColEI; M13 phage; gene III; fusion protein; lambda; recombinase; int;
 KM phagemid; ss.
 XX
 OS Synthetic.
 XX
 PM FR2715940-A1.
 XX
 PD 11-AUG-1995.
 XX
 PF 10-FEB-1994; 94FR-00001519.
 XX
 PR 10-FEB-1994; 94FR-00001519.
 XX
 PA (INMR) PASTEUR MERIEUX SERUMS & VACCINS.
 XX
 PI Sodoyer R, Aujame L, Geoffroy F;
 XX
 DR WPI; 1995-277038/37.
 XX
 PT Prepn. of multi-combinatorial vector library expressing antibody
 PT fragment(s) - by recombination of vector(s) contg., separately, genes for
 PT light and heavy chain variable region(s).
 XX
 PS Example 2; Page 25; 39pp; French.

The preparation of a multicombinatorial vector library expressing
 fragment of antibodies is carried out by recombining two vectors each
 contg. separately the gene encoding an antibody light or heavy chain
 variable region. The vectors contg the light chain variable region are
 derived from the plasmid pACYC177 and contain the kanamycin resistance
 gene and the p15a origin of replication, the lac promoter from
 pBluescript, the peltB signal sequence and the chloramphenicol resistance
 gene from pBR328. The gene encoding the light chain variable region is
 inserted in frame with the peltB signal sequence to produce the plasmid
 pM87. The vector expressing the heavy chain variable region is derived
 from the plasmid pBluescript SKI+ and contains the ampicillin resistance
 gene and the ColEI origin of replication from that plasmid. The plasmid
 has inserted the peltB signal sequence and the sequence encoding the gene
 III product from M13 phage. The gene encoding the heavy chain variable
 region is inserted in frame with the M13 gene III sequence so as to
 produce a fusion product. The heavy chain vector is designated pM82.
 Both plasmids contain recombination sites: the light chain vector
 contains the lambda attB site whilst the heavy chain vector contains the
 attP site. When introduced into a suitable host cell and contacted by the
 recombinase protein int, the two vector recombine to produce the 8.6 kb
 recombinant phagemid pM85. This vector forms the basis of the library.
 The primers AAQ95082-3 are used to amplify a 663 bp fragment of the
 sequence encoding the gene III protein from the phage M13 mp18 (bases
 2223-2885). The resultant fragment is inserted into pM82 to generate the
 plasmid pM830. The method can be used to produce a library which contains
 a higher number of antibody light and heavy chain clones

Sequence 39 BP; 5 A; 7 C; 14 G; 13 T; 0 U; 0 Other;

Query Match 4.3%; Score 18; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
 |||||
 Db 27 ATGAGAGCCACCGCCAC 10

RESULT 3
 AAQ78813/c
 ID AAQ78813 standard; DNA; 48 BP.
 XX
 AC AAQ78813;
 XX
 DT 25-MAR-2003 (revised)
 XX
 DE Membrane anchor domain cpiII PCR primer G-3(F).
 XX
 KM Bacteriophage coat protein; membrane anchor domain cpiII; HMCV;
 KM human cytomegalovirus; antibody; immunoassay; immunotherapy; PCR primer;
 KM ss.
 XX
 OS Synthetic.
 XX
 PM WO9425490-A1.
 XX
 PD 10-NOV-1994.
 XX
 PF 29-APR-1994; 94WO-US004705.
 XX
 PR 30-APR-1993; 93US-00055985.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Burton DR, Barbas C, Burton R, Williamson A;
 XX
 DR WPI; 1994-358194/44.
 XX
 PT Human monoclonal antibodies (MAbs) against human cytomegalovirus - also
 PT nucleic acids and cell lines producing the MAbs, useful in diagnosis and
 PT immunotherapy.
 XX
 PS Example 1b1; Page 76; 171pp; English.

AAQ78813 and AAQ78814 are a pair of primers for the PCR amplification of
 CC AAQ78812, which encodes AAR62927 bacteriophage coat protein membrane
 CC anchor domain cpiII. It was used in the construction of an expression
 CC vector for a human cytomegalovirus (HMCV) monoclonal antibody (Mab). The
 CC Mab could be used to detect HCMV, and anti-human HCMV Abs in human
 CC patients via a competitive immunoassay. The Mabs may also be useful in
 CC immunotherapy. (Updated on 25-MAR-2003 to correct FN field.)
 XX

Sequence 48 BP; 10 A; 9 C; 15 G; 14 T; 0 U; 0 Other;

Query Match 4.3%; Score 18; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
 |||||
 Db 31 ATGAGAGCCACCGCCAC 14

RESULT 4
 AAQ64223/c
 ID AAQ64223 standard; DNA; 48 BP.
 XX
 AC AAQ64223;

```

DE PCR primer G-3(F) to clone membrane anchor domain of M13 cpIII.
XX
XX Human immunodeficiency virus; HIV1; glycoprotein; epitope;
XX neutralisation; monoclonal antibody; light chain; variable region;
KM filamentous phage M13; M13mp18; coat protein cpIII; PCR;
KW polymerase chain reaction amplification; ss.
XX
OS Synthetic.
XX
PM WO9407922-A1.
XX
PD 14-APR-1994.
XX
PF 30-SEP-1993; 93WO-US009328.
XX
PR 30-SEP-1992; 92US-00954148.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Burton DR, Barbas CF, Lerner RA;
XX
PP WPI; 1994-135516/16.
XX
PT New human monoclonal antibodies neutralising HIV - react with gp120 or
PT gp121 and nucleic acid encoding them, useful for in vivo or in vitro
PT diagnosis and for passive immuno-therapy.
XX
XX Example 1; Page 146; 248pp; English.
XX
PS M13mp18 replicative form DNA was used as a template for isolating the
CC gene encoding the membrane anchor domain at cpIII. Two PCR amplifications
CC were performed for construction of a DNA fragment consisting of the
CC mature gene for cpIII membrane anchor domain located 5' to a sequence
CC encoding the lacZ promoter, operator and cap-binding site for controlling
CQ light chain expression. Primers G-3(F) and G-3(B) (AAQ64223 and AAQ64224,
CC respectively) were used for the first PCR amplification. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 48 BP; 10 A; 9 C; 15 G; 14 T; 0 U; 0 Other;
'
Query Match 4.3%; Score 18; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0
CY 67 ATGGAGAGCCACCGCCAC 84
   |||||
DB 31 ATGGAGAGCCACCGCCAC 14

```

XX	04-JAN-1994;	94US-00178201.
PR	(SCRI) SCRIPPS RES INST.	
PA	Burton DR, Williamson RA, Burioni R, Sanna PP;	
XX	WPI; 1995-254909/33.	
DR		
XX		
PT	Human monoclonal antibodies that neutralise Herpes simplex virus (HSV)	
PT	types 1 and 2 - used for diagnosis and passive immuno-therapy of HSV	
PT	infections.	
XX		
PS	Example 1; Page 81, 100pp; English.	
XX		
CC	AAG94730 and AAG94731 are PCR primers used to amplify the gpII membrane	
CC	anchor gene which is used in part of a process which produces a plasmid	
CC	pComb-IIIT. pCombIIIT'is a bacteriophage vector used to identify human	
CC	pComb-IIIT. pCombIIIT'is a bacteriophage vector used to identify human	
CC	monoclonal antibodies that immunoreact with HSV. One such antibody is the	
CC	human anti-herpes monoclonal antibody clone FabHsv8. This antibody is	
CC	capable of neutralising both herpes simplex virus (HSV) types I and II by	
CC	binding an epitope present on glycoprotein D. The antibody may be used	
CC	for detecting HSV in vivo or in vitro; for passive immunotherapy (pref.	
CC	phorphyllactically) of HSV infection (eg. genital, oral or ocular herpes),	
CC	partic, as its Fab fragment and as a competitive reagent for detecting	
CC	neutralising anti-HSV antibodies in a sample. Anti-idiotypic antibodies	
CC	raised against the mAb can be used for active immunotherapy of HSV	
CC	infection. (Updated on 16-OCT-2003 to standardise OS field)	
XX		
SQ	Sequence 48 BP; 10 A; 9 C; 15 G; 14 T; 0 U; 0 Other;	
	Query Match	4.3%; Score 18; DB 2; Length 48;
	Best Local Similarity	100.0%; Pred.No.1e+02;
	Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	67 ATGAGAGGCCACCGCCAC 84	
Db	31 ATGAGAGGCCACCGCCAC 14	
RESULT 6		
AT40878/c		
ID	AA40878 standard; DNA; 48 BP.	
XX		
AC	AA40878;	
XX		
DT	28-JAN-1997 (first entry)	
DE	pComb2-3 construction primer, G-3(F).	
XX		
KM	Heavy chain; light chain; variable region; VH; monoclonal antibody; Mab;	
KW	HIV; human immunodeficiency virus; glycoprotein; gp120; clone;	
KM	virus infectivity assay; precursor gp160; immunocompetence; VL; human;	
XX	anti-HIV antibody; detection; HIV infection; ss.	
OS	Synthetic.	
PN	WO9602273-A1.	
PD	01-FEB-1996.	
PF	11-JUL-1995; 95WO-US008743.	
PR	18-JUL-1994; 94US-00276852.	
FA	(SCRI) SCRIPPS RES INST.	
P1	Burton DR, Barbas CF, Lerner RA;	
DR	WPI; 1996-179601/18.	
PT	Mono-clonal antibody binding to V1/V2 loop of HIV gp120 - used in passive	
PT	immuno-therapy and detection of HIV infection.	

CC sequences from the host cell. The anti-HIV gp-120 monoclonal antibody is
CC used for providing passive immunotherapy to HIV in a human. They can be
CC administered to high-risk patients to reduce the likelihood and/or
CC severity of HIV-induced disease and to patients who are already HIV-
CC infected. The antibodies are used for neutralising field isolates which
CC provide information about the immunocompetence of an immune response in
CC HIV patients, for detecting HIV in a biological fluid or tissue sample
CC e.g. by radioimmunoassay, for producing anti-idiotypic antibodies which
CC can be used for active immunisation and to screen human monoclonal
CC antibodies to identify those with the same binding specificity and to
CC monitor the course of HIV disease therapy by measuring the changes in
CC concentration of HIV present in the body or in body fluids by
CC immunosay. The anti-HIV gp-120 monoclonal antibodies are encoded by a
CC human polynucleotide sequence and when used in vivo for diagnosis and
CC immunotherapy of HIV-induced disease reduce the problems of significant
CC host immune response to the antibodies associated with monoclonal
CC antibodies of xenogeneic or chimeric derivation

CC Sequence 48 BP; 10 A; 9 C; 15 G; 14 T; 0 U; 0 Other;

Query Match 4.3%; Score 18; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
DB 31 ATGAGAGCCACCGCCAC 14

RESULT 9

AAA30998/c
ID AAA30998 standard; DNA; 48 BP.

AC AAA30998;

DT 30-JUN-2000 (first entry)

DE Primer G-3 F used in the preparation of pComBIII.

CC Anti-human immunodeficiency virus type 1 antibody; HIV-1; neutralise;
CC reduce HIV infection; diagnosis; immunotherapy; HIV induced disease; ss;
CC glycoprotein 120; gp120; glycoprotein 41; gp41; monoclonal antibody.

OS Synthetic.

BN AU9948756-A.

XX 17-FEB-2000.

PD 16-SEP-1999; 99AU-00048756.

PF 16-SEP-1999; 99AU-00048756.

PR (SCRI) SCRIPPS RES INST.

PA Burton DR, Barbas CF, Lerner RA;

PI WPI; 2000-293393/26.

CC Novel human monoclonal antibodies which immunoreact with and neutralize
CC human immunodeficiency virus useful for treating HIV infections.

CC Example 1; Page 76; 366pp; English.

CC The present sequence is used in the production of anti-human
CC immunodeficiency virus type 1 (HIV-1) antibodies. The invention relates
CC to a human whole immunoglobulin (Ig) molecule which immunoreacts with HIV
CC mature glycoprotein gp120 preferentially over HIV precursor glycoprotein
CC gp160 and neutralises HIV and which reduces HIV infectivity titre in an
CC in vitro virus infectivity assay by 50%, at a concentration of less than
CC 700 ng/ml. The antibodies are used as reagents for the diagnosis and
CC immunotherapy of HIV induced disease. They are useful as neutralising
CC field isolates and provide useful information regarding the

CC immunocompetence of an immune response in HIV infected patients. The
CC monoclonal antibodies are useful for producing anti-idiotypic antibodies
CC which can be used to screen human monoclonal antibodies to identify
CC whether the antibody has the same binding specificity as the antibodies
CC of the invention. The neutralising antibodies define new epitopes on the
CC HIV gp120 and gp41 glycoproteins, thus increasing the availability of new
CC immunotherapeutic human monoclonal antibodies. A major advantage of the
CC monoclonal antibodies derives from the fact that they are encoded by a
CC human polynucleotide sequence. Thus in vivo use of the monoclonal
CC antibodies for diagnosis and immunotherapy of HIV induced disease greatly
CC reduces the problems of significant host immune response to the passively
CC administered antibodies which is a problem commonly encountered when
CC monoclonal antibodies of xenogeneic or chimeric derivation are utilized.
CC An additional major advantage of the monoclonal antibodies described
CC derives from the fact that they immunoreact with a unique determinant
CC present on mature HIV glycoprotein gp120. This class of antibodies is
CC particularly effective at neutralising field isolates of HIV

CC Sequence 48 BP; 10 A; 9 C; 15 G; 14 T; 0 U; 0 Other;

Query Match 4.3%; Score 18; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
DB 31 ATGAGAGCCACCGCCAC 14

RESULT 10

AAL38725/c
ID AAL38725 standard; DNA; 48 BP.

AC AAL38725;

DT 02-SEP-2002 (first entry)

DE cPIII membrane anchor gene PCR primer SEQ ID No 19.

CC Antibody; epitope; solid support; phage display combinatorial antibody;
CC immunocomplex; antigen; PCR; primer; ss.

OS Unidentified.

BN US6376170-B1.

XX 23-APR-2002.

PD 18-NOV-1997; 97US-00972564.

PF 03-OCT-1994; 94US-00316914.

PR (SCRI) SCRIPPS RES INST.

PA Burton DR, Burioni R, Williamson RA, Sanna PP;

PI WPI; 2002-478279/51.

CC Obtaining antibody that binds to previously unknown epitope on antigen
CC using solid phase capture complex of known antibody-antigen, is useful to
CC screen e.g. phage display combinatorial libraries.

CC Example 1; Col 22; 27pp; English.

CC The invention relates to a novel method for obtaining an antibody that
CC binds to a previously unknown epitope on a preselected antigen, which
CC comprises contacting the preselected antigen with a specific antibody
CC bound to a solid support, contacting the formed immunocomplex with a
CC combinatorial library of antibodies so that a second antibody binds to a
CC previously unknown epitope, and removing the second antibody. The method
CC is used to screen libraries of cloned antibodies, such as phage display
CC combinatorial antibodies. This polynucleotide sequence represents a PCR
CC primer relating to the invention

XX Sequence 48 BP; 10 A; 9 C; 15 G; 14 T; 0 U; 0 Other;
SQ
Query Match 4.3%; Score 18; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
67 ATGAGAGACCAAGCCGAC 84
31 ATGAGAGACCAAGCCGAC 14
Db
RESULT 11
ADB84272/c
ID ADB84272 standard; DNA; 48 BP.
XX
AC ADB84272;
XX
DT 04-DEC-2003 (first entry)
XX
DE Disciption expression vector associated primer #19.
XX
KW antibody identification; phage display combinatorial library;
KM disciption expression vector; heterodimeric receptor expression;
XX Fab antibody; PCR; primer; ss.
XX
CQ Synthetic.
XX
PN US2002168629-A1.
XX
PD 14-NOV-2002.
XX
PF 19-FEB-2002; 2002US-00079802.
XX
PR 03-OCT-1994; 94US-00316914.
PR 18-NOV-1997; 97US-00972564.
XX
PA (SCRI) SCRIIPS RES INST.
PI Burton DR, Burioni R, Williamson RA, Sanna PP;
XX
DR WPI; 2003-719983/68.
XX
PT Identifying an antibody that binds an unmasked epitope on a preselected
PT antigen e.g. for panning using phage display combinatorial libraries;
PT comprises contacting a second antibody with an antigen and first antibody
PT immunocomplex.
XX
PS Example 1; Page 12; 29pp; English.
XX
CC The invention describes a method of identifying an antibody that binds to
CC an unmasked epitope on a preselected antigen (I), by: (a) contacting (I)
CC with an antibody (II), under conditions which allow a first epitope of
CC (I) to bind to (II) and form an immunocomplex; (b) contacting a second
CC antibody molecule (III) with a complex so that (III) binds to a second,
CC unmasked epitope on (I); and (c) removing (III) bound to the second
CC epitope. The method is useful for identifying an antibody molecule that
CC binds to an unmasked epitope on (I), having a preselected first epitope
CC and (I) additional epitope. The method is useful for crude cell or viral
CC lysates containing antigens of interest and for panning using phage
CC display combinatorial libraries. The method allows more accurate
CC selection of antibodies. This sequence represents a primer used in the
CC construction of a disciption expression vector for production of
CC heterodimeric receptor molecules on phage particles for production of a
CC large number of Fab antibody fragments that can be screened directly.
XX
SQ Sequence 48 BP; 10 A; 9 C; 15 G; 14 T; 0 U; 0 Other;
Query Match 4.3%; Score 18; DB 8; Length 48;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
67 ATGAGAGACCAAGCCGAC 84

Db
31 ATGAGAGACCAAGCCGAC 14
RESULT 12
ABN38420
ID ABN38420 standard; DNA; 60 BP.
XX
AC ABN38420;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:11168.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KM splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-1B001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUSEN INC.
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 11168; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of tissue
CC - and pathological-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
SQ Sequence 60 BP; 15 A; 16 C; 17 G; 12 T; 0 U; 0 Other;
Query Match 4.1%; Score 17; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
390 GAACCTCAGGCTCTGG 406

DB 37 GAACCTCAGGCTCTGG 53

RESULT 13

AA18458
ID AAX18458 standard; DNA; 66 BP.

XX
XX AAX18458;
AC
XX
XX 13-MAY-1999 (first entry)
DT
XX
DE PCR primer tau3-1 used in construction of h1FNtau3C coding sequence.
XX
XX Interferon tau3; human, h1FNtau3C; antitumour agent; autoimmune disease;
KM antiviral activity; therapy; PCR primer; ss.
XX
XX
OS Synthetic.
XX Homo sapiens.
XX JPI1042089-A.
XX
XX 16-FEB-1999.
PD
XX 29-JUL-1997; 97JP-00203137.
PF
XX 29-JUL-1997; 97JP-00203137.
PR
XX 29-JUL-1997; 97JP-00203137.
XX
XX (SANY) SANKYO CO LTD.
PA
XX WPI; 1999-197821/17.
DR
XX
XX An interferon tau 3 modified body protein and polynucleotide - useful for
PT treatment of autoimmune diseases, and in antitumor agents.
XX
XX Disclousure; Page 6; 18pp; Japanese.
PS
XX This sequence represents a primer used in the construction of DNA
CG encoding the modified human interferon tau 3 protein of the invention,
CC designated h1FNtau3C. h1FNtau3C is useful as an antitumour agent, and for
CC treatment of autoimmune diseases. The interferon tau 3 modified body
CC h1FNtau3C has a high antiviral activity and is low in cytotoxicity
XX
XX
SQ Sequence 66 BP; 14 A; 19 C; 19 G; 14 T; 0 U; 0 Other;

Query Match 4.1%; Score 17; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 390 GAACCTCAGGCTCTGG 406
DB 42 GAACCTCAGGCTCTGG 58

RESULT 14

AB261630
ID AB261630 standard; RNA; 17 BP.

XX
XX AB261630;
AC
XX
XX 21-MAR-2003 (first entry)
DT
XX
XX Human H-Ras DNAzyme target #421.
DE
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KM anti-rheumatic; cancer; AIDS; ss.
XX
XX
OS Homo sapiens.
XX
XX WO200297114-A2.
PN
XX
XX 05-DEC-2002.
PD
XX

PF 23-MAY-2002; 2002WO-US016840.
XX
XX 23-MAY-2001; 2001US-0294140P.
PR
XX 06-JUN-2001; 2001US-0296249P.
PR
XX 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX
PI Mcswiggen U;
PS
XX WPI; 2003-140484/13.
DR
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer; modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX
PS Claim 58; Page 119; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in AB259889 - AB262216, AB264544 - AB265531, AB265520 - AB265524,
CC AB265530 - AB265585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
XX
SQ Sequence 17 BP; 4 A; 6 C; 6 G; 0 T; 1 U; 0 Other;

Query Match 3.6%; Score 15; DB 7; Length 17;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 194 ACAGCGCCATCGCGG 208
DB 1 ACAGCGCCATCGCGG 15

RESULT 15

AAV85968/C
ID AAV85968 standard; DNA; 20 BP.

XX
XX AAV85968;
AC
XX
XX 10-FEB-1999 (first entry)
DT
XX
XX Mouse LRP-3 cDNA PCR primer 414r (MUCD 7R).
DE
XX
XX LRP5; LDL-receptor related protein; LRP-3; IDDM; diagnosis; endocytosis;
KM insulin dependent diabetes mellitus; autoimmune disease;
KM glomerulonephritis; inflammation; viral infection; osteoporosis;
KM hypercholesterolemia; Alzheimer's disease; low density lipoprotein;
KM PCR primer; ss.
XX
XX
XX Synthetic.
OS
XX
XX Mus sp.
XX
XX WO9846743-A1.
XX
XX 22-OCT-1998.
PD
XX
XX 15-APR-1998; 98WO-GB001102.
PF
XX
XX 15-APR-1997; 97US-0043553P.
PR
XX 05-JUN-1997; 97US-0048740P.
XX
XX (WELL) WELLCOME TRUST LTD.
PA
XX (MERI) MERCK & CO INC.
XX

PI Todd JA, Hess JM, Caskey CT, Cox RD, Gerhold D, Hammond H,
 PI Hey P, Kawaguchi Y, Merriman TR, Metzker ML, Nakagawa Y,
 PI Phillips MS, Twells RCJ;

DR MPI; 1998-594573/50.

PT New isolated LDL-receptor related protein - used to develop products for
 PT treating, e.g. elevated triglyceride levels, diabetes, autoimmune
 PT disorders, inflammation or Alzheimer's disease.

PS Claim 12; Page 117; 2000p; English.

XX The present invention describes LRP5 (low density lipoprotein (LDL)
 CC receptor related protein, previously designated LRP-3). Nucleic acid
 CC molecules (NMs) encoding LRP5 can be used for determining if an
 CC individual is susceptible to insulin dependent diabetes mellitus (IDDM).
 CC The NMs or proteins can be used for reducing triglyceride levels in the
 CC serum of an individual. Therapies that affect LRP5 may also be useful in
 CC the treatment of autoimmune diseases such as glomerulonephritis, diseases
 CC and disorders involving disruption of endocytosis and/or antigen
 CC presentation, cytokine clearance and/or inflammation, viral infection,
 CC pathogenic bacterial toxin contamination, elevation of free fatty acids
 CC or hypercholesterolemia, type 2 diabetes, osteoporosis, Alzheimer's
 CC disease and cardiovascular disease. Products from the present invention
 CC can also be used for detection, diagnosis and drug screening. AAV85917 to
 CC AAV86012 represent PCR primers for obtaining LRP-3 cDNA

XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 3.6%; Score 15; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;

-Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 GGAGTGTCTGCACAG 179

DB 20 GGAGTGTCTGCACAG 6

Search completed: March 22, 2004, 03:30:38
 Job time : 395 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 23:24:50 ; Search time 2999 Seconds

(without alignments)
6026.691 Million cell updates/sec

Title: US-10-032-159A-15

Perfect score: 417
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Searched: 3470272 seqs, 21671516995 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

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2: gb_hcg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
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41: gb_ov:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	351	84.2	2621	9	BC018142	BC018142 Homo sapi
2	351	84.2	3682	6	AY032927	AY032927 Homo sapi
3	351	84.2	3766	6	AX746790	AX746790 Sequence
4	351	84.2	3766	6	AX091123	AX091123 Homo sapi
5	351	84.2	3931	9	AF322642	AF322642 Homo sapi
6	212	50.8	55173	2	AC132816	AC132816 Homo sapi
7	212	50.8	144000	9	AC123764	AC123764 Homo sapi
8	212	50.8	182016	9	AC087741	AC087741 Homo sapi
9	212	50.8	187865	2	AC015559	AC015559 Homo sapi
10	212	50.8	207822	2	AC109321	AC109321 Homo sapi
11	205	49.2	55173	2	AC132816	AC132816 Homo sapi
12	161	38.6	74301	2	AC137736	AC137736 Homo sapi
13	13	7.9	3772	10	AF363457	AF363457 Mus muscu
14	14	7.9	3995	10	BC029102	BC029102 Mus muscu
15	15	7.9	24653	10	AL645911	AL645911 Mouse DNA
16	23	5.5	3164	10	BC004692	BC004692 Mus muscu
17	22	5.3	160170	2	AP001158	AP001158 Homo sapi
18	22	5.3	221941	9	AC091060	AC091060 Homo sapi
19	22	5.3	224788	2	AP001905	AP001905 Homo sapi
20	21	5.0	1260	10	AB010281	AB010281 Mus muscu
21	21	5.0	4085	10	AY135367	AY135367 Mus muscu
22	21	5.0	65608	2	AC132197	AC132197 Homo sapi
23	21	5.0	110000	2	LMFLCHR36_24	Continuation (25 o
24	21	5.0	165614	10	AC111044	AC111044 Mus muscu
25	21	5.0	182626	2	AC124374	AC124374 Mus muscu
26	21	5.0	225027	2	AC131725	AC131725 Mus muscu
27	21	5.0	239392	2	AC115417	AC115417 Rattus no
28	21	5.0	245032	2	AC109749	AC109749 Rattus no
29	21	4.8	45013	9	AL138684	AL138684 Human DNA
30	20	4.8	53730	9	AC135726	AC135726 Homo sapi
31	20	4.8	135351	2	AC068279	AC068279 Homo sapi
32	20	4.8	150469	2	AC068854	AC068854 Homo sapi
33	20	4.8	165028	9	AC110758	AC110758 Homo sapi
34	20	4.8	183176	2	AC106894	AC106894 Homo sapi
35	20	4.8	191947	2	AC135875	AC135875 Rattus no
36	20	4.8	192181	9	AC133644	AC133644 Homo sapi
37	20	4.8	201764	2	AL359818	AL359818 Homo sapi
38	20	4.8	202312	2	AC135269	AC135269 Rattus no
39	20	4.8	204006	2	AC134881	AC134881 Homo sapi
40	20	4.8	205662	9	AC017002	AC017002 Homo sapi
41	20	4.8	214361	2	AC105814	AC105814 Rattus no
42	20	4.8	229276	2	AC120704	AC120704 Rattus no
43	20	4.8	240214	2	AC126871	AC126871 Rattus no
44	20	4.8	283969	2	AC120737	AC120737 Rattus no
45	19	4.6	2294	10	BC004088	BC004088 Mus muscu

ALIGNMENTS

RESULT 1
LOCUS BC018142 2621 bp mRNA linear PRI 03-OCT-2003
DEFINITION Homo sapiens caspase recruitment domain family, member 14, mRNA
(CDNA clone MGC:9539 IMAGE:3847282), complete cds.

ACCESSION BC018142
VERSION BC018142.1 GI:117390314

KEYWORDS MGC.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2621)
Strausberg,R.L., Feingold,B.A., Grouse,J.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Pred. No. is the number of results predicted by chance to have a

JOURNAL	FRES Lett.	496 (2-3), 121-127 (2001)
MEDLINE	21255663	
PUBMED	11356195	
REFERENCE	2 (bases 1 to 3682)	
AUTHORS	Marthon, F., Thome, M. and Teschopp, J.	
TITLE	Direct Submersion	
JOURNAL	Submitted (23-APR-2001) Institute of Biochemistry, University of	
	Lausanne, Ch. des Boveresses 155, Epalinges, VD 1066, Switzerland	
FEATURES		
Source	1..3682	

ORIGIN	Query Match	84.2%	Score 351	DB 9	Length 3682	
	Best Local Similarity	100.0%	Pred. No. 2.7e-170	Mismatches 0	Indels 0	Gaps 0
	Matches 351	Conservative	0			
QY	1	ATGGGGAAACTGTGCGCGCAGAGACTTCGCACTCCAGCAACGCACTGCAACGAGAGACACTGTGG	60			
DB	4	ATGGGGGAACTGTGCGCGCAGAGACTTCGCACTCCAGCACTCCAGCAACGAGAGACACTGTGG	63			
QY	61	GAGATGATGAGAGGCCACCGCCACAGAGATGTAAGCTGATCTTGCCCAAGCGCTCAAC	120			
DB	64	GAGATGATGAGAGGCCACCGCCACAGAGATGTAAGCTGATCTTGCCCAAGCGCTCAAC	123			
QY	121	CCCTTACCTGCGCCAGGCGCAAGTGTCTGTCTCCAGCTGGAAGAGAGAGAGTGTCTGCACAC	180			
DB	124	CCCTTACCTGCGCGCCAGGCGCAAGTGTCTGTCTCCAGCTGGAAGAGAGAGAGTGTCTGCACAC	183			
QY	181	CCCGGCGCTACCAACAGCGCCATGCGGGCGCGGCACTTCTGGATTGCTGAAGACTCGA	240			
DB	184	CCCGGCGCTACCAACAGCGCCATGCGGGCGCGGCACTTGTGATTGCTGAAGACTCGA	243			
QY	241	GGGAAGAACGGGGGCATCGCTTCTCTGAGAGCGCTGAAGTTCACAAACCTGACGCTTAC	300			
DB	244	GGGAAGAACGGGGGCATCGCTTCTCTGAGAGCGCTGAAGTTCACAAACCTGACGCTTAC	303			
QY	301	ACCCTGTGTCACGGGCTGCAAGCTGATGTTGACTTCACTGAACCTTTAGCGGT	351			
DB	304	ACCCTGTGTCACGGGCTGCAAGCTGATGTTGACTTCACTGAACCTTTAGCGGT	354			

```

RESULT 3
AX746790
LOCUS AX746790 3766 bp mRNA linear PAT 20-JUN-2003
DEFINITION Sequence 315 from Patent EP1308459.
ACCESSION AX746790
VERSION
KEYWORDS
ORGANISM
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yanamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tameshika,I., Seki,N., Yoshikawa,T., Otsuka,M., Negahari,K. and
Masuko,Y.
Full-length cDNA sequences
Patent: EP 1308459-A 315 07-MAY-2003;
Helix Research Institute (JP) ; Research Association for
Biotechnology (JP)
FEATURES
Source
Location/Qualifiers
1..3766
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
ORIGIN

```

	Query Match	84.2%	Score 351;	DB 6;	Length 3766;	
	Best Local Similarity	100.0%;	Pred.	No. 2.7e-170;		
	Matches 351;	Conservative	0;	Mismatches	0;	Gaps 0.
QY	1 ATGGGAGAACTGTGCACCGCAGGAGACTCCGCCATCTCAAGGACACTGGA CGA GAGACA CTGTGG	60				
Db	192 ATGGGGAGACTGTGTCGGAGGACTCCGCCATCTCAAGGACACTGGA CGA GAGACA CTGTGG	251				
QY	61 GAGATGATGAGAGAGCCACCGCACAGATGTAAGCTGCATCTGCCAGCCGCTCAC	120				
Db	252 GAGATGATGAGAGAGCCACCGCACAGATGTAAGCTGCATCTGCCAGCCGCTGCAC	311				
QY	121 CCTTACCTCGCCGACGAGCCCAAGGTGTGTGCGACCTGGACGAGGAGAGAGTGCTGCACGC	180				
Db	312 CCTTACCTCGCCGACGAGCCCAAGGTGTGTGCGACCTGGACGAGGAGAGAGTGCTGCACGC	371				
QY	181 CCCCAGGCTCACCAACAGCGCATGCGGAGCCGGGCACTTGCTGATTTGCTGAAGA CTGCA	240				
Db	372 CCCCAGGCTCACCAACAGCGCATGCGGAGCCGGGCACTTGCTGATTTGCTGAAGA CTGCA	431				
QY	241 GGGAAGAACGGGGCCATGCGCTTCTCTGGAGAGCCTGAAGTTCCACAACCCTGACGCTTAC	300				
Db	432 GGGAAGAACGGGGCCATGCGCTTCTCTGGAGAGCCTGAAGTTCCACAACCCTGACGCTTAC	491				
QY	301 ACCCTGTGTCAACCGGCTGTGACAGCTTGTACATTGACATTCTTAAGCGGT	351				
Db	492 ACCCTGTGTCAACCGGCTGTGACAGCTTGTACATTGACATTCTTAAGCGGT	542				
RESULT 4						
AKO91123	3766 bp mRNA linear PRI 15-JUL-2000					
LOCUS	Homo sapiens cDNA FLJ3804 f.1, clone CHONG2000766, weakly similar					
DEFINITION	to Rattus norvegicus caspase recruitment domain protein 9 mRNA.					
AKO91123						
ACCESSION	AKO91123.1 GI:21749418					
VERSION	oligo capding; f.1s (full insert sequence).					
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
REFERENCE						
AUTHORS	1 Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T., Shiohara, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R., Yoshikawa, Y., Matsunura, Y., Moriya, S., Chiba, E., Momiyama, H., Onogawa, S., Kaeriyama, S., Satoh, N., Matsunawa, H., Takahashi, E.,					

Db	327	CCCTACCTGGCCACAGGCCAAGTGTGTGTGCACAGTCGACGAGAGAGAGAGTGTGTGCACAGC	386
Qy	181	CCCCGGCTCACCAACAGCGCCATGCGGGCCCGGCACTTGTGGATTGTCTGAAGACTCGA	240
Db	387	CCCCGGCTCAACCAACAGCGCCATGCGGGCCCGGCACTTGTGGATTGTCTGAAGACTCGA	446
Qy	241	GGGAAGAACGGGGCATGCGCTTCTCTGAGAGCCTGAAGTTCCAAACCTGACGCTTAC	300
Db	447	GGGAAGAACGGGGCCATGCGCTTCTCTGAGAGCCTGAAGTTCCAAACCTGACGCTTAC	506
Qy	301	ACCCGTGTCACCGGGCTGACGCTCATTTGACTTCAGTTAACTTTAGCGGT	351
Db	507	ACCCGTGTCACCGGGCTGACGCTCATTTGACTTCAGTTAACTTTAGCGGT	557

RESULT 6	AC132816	55173 bp	DNA	linear	HTG 04-SEP-2007
LOCUS	AC132816				
DEFINITION	Homo sapiens chromosome 17 clone RP13-593A24 map 17, LOW-PASS SEQUENCE SAMPLING.				
ACCESSION	AC132816				
VERSION	AC132816.1	GI:22711605			
KEYWORDS	HTG; HTGS; PHASE0.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1 (bases 1 to 55173)
Birtten,B., Nusbäum,C. and Lander,E.
Homo sapiens chromosome 17, clone RP13-593A24
Unpublished
2 (bases 1 to 55173)
Birtten,B., Nusbäum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,

TITLE Direct Submission
JOURNAL Submitted (04-SEP-2002) Whitehead Institute/MIT Center for Genomewide Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT All repeats were identified using RepeatMasker:

* NOTE: This record contains 70 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone

Genome Center
 Center: Whitehead Institute / MIT Center for Genome Research
 Center code: WIRB
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: I28179
 Center clone name: 593_A_24

* will be sequenced to completion. In the event that		
* the record is updated, the accession number will		
* be preserved.		
1	692: contig of 692 bp	in length
693	792: gap of 100 bp	
793	1579: contig of 687 bp	in length
1480	1579: gap of 100 bp	
1580	2271: contig of 652 bp	in length
2272	2371: gap of 100 bp	
2372	3056: contig of 685 bp	in length
3057	3156: gap of 100 bp	
3157	3858: contig of 702 bp	in length
3859	3588: gap of 100 bp	
3959	4532: contig of 674 bp	in length
4633	4732: gap of 100 bp	
4733	5518: contig of 686 bp	in length
5419	5518: gap of 100 bp	
5519	6199: contig of 681 bp	in length
6200	6299: gap of 100 bp	
6300	6696: contig of 670 bp	in length
6570	7069: gap of 100 bp	
7070	7779: contig of 710 bp	in length
7780	7879: gap of 100 bp	
7880	8568: contig of 689 bp	in length
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8669	9364: contig of 696 bp	in length
9365	9464: gap of 100 bp	
9465	10171: contig of 707 bp	in length
10172	10271: gap of 100 bp	
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10964	10963: gap of 100 bp	
11064	11751: contig of 668 bp	in length
11552	11651: gap of 100 bp	
11852	12547: contig of 656 bp	in length
12548	12647: gap of 100 bp	
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13310	13409: gap of 100 bp	
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14099	14198: gap of 100 bp	
14199	14669: contig of 671 bp	in length
14870	14969: gap of 100 bp	
14870	15667: contig of 658 bp	in length
15668	15767: gap of 100 bp	
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16480	16579: gap of 100 bp	
16580	17268: contig of 689 bp	in length
17269	17368: gap of 100 bp	
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18139	18829: contig of 691 bp	in length
18830	18829: gap of 100 bp	
18830	19632: contig of 703 bp	in length
19633	19732: gap of 100 bp	
19733	20432: contig of 700 bp	in length
20433	20532: gap of 100 bp	
20533	21213: contig of 681 bp	in length
21214	21313: gap of 100 bp	
21314	21968: contig of 675 bp	in length
21969	22088: gap of 100 bp	
22089	22801: contig of 713 bp	in length
22802	22901: gap of 100 bp	
22902	23575: contig of 674 bp	in length
23576	23675: gap of 100 bp	
23676	24355: contig of 680 bp	in length
24356	24455: gap of 100 bp	
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25147	25246: gap of 100 bp	
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25948	26047: gap of 100 bp	
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* 38653 38752: gap of 100 bp
* 38753 39440: contig of 688 bp in length
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* 41016 41115: gap of 100 bp
* 41116 41820: contig of 705 bp in length
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* 48170 48847: contig of 678 bp in length
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* 49637 49737: gap of 100 bp
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* 51214 51313: gap of 100 bp
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* 54478 55173: gap of 100 bp
* 55173 55173: contig of 696 bp in length.

```

FEATURES

Query Match

50.8%; Score 212; DB 2; Length 55173;

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Best Local Similarity 100.0%; Pred. No. 1.6e-98;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 51604 ATGGGGAAGTGTGGCCGAGGAGTCCGACTCAGCAGTGTGAGAGACACTGTGG 51663
QY 61 GAGATGATGAGAGACGACCGCCAGAGATGTGTAGCGTGCATCTGCCAGCGCTCACC 120
Db 51664 GAGATGATGAGAGACGACCGCCAGAGATGTGTAGCGTGCATCTGCCAGCGCTCACC 51723
QY 121 CCTACTCTGGCCGAGGAGGAGAGTGTGTGCGAGCTGTGAGAGAGAGAGTGTGTGACAGC 180
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RESULT 7
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LOCUS Homo sapiens chromosome 17, clone CTC-784N20, complete sequence.
DEFINITION AC123764
ACCESSION AC123764
VERSION AC123764.18 GI:28913166
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

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REFERENCE 1 (bases 1 to 144000)
Birken, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone CTC-784N20
Unpublished
2 (bases 1 to 144000)
Birken, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
Bouhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collamore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Gord, S., Govette, M., Graham, L.,
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Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lacombe, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,
Liu, G., Maclean, C., Macdonald, P., Major, J., Margulis, N.,
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Nicot, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Punnkham, M., Riley, R., Rise, C.,
Pollara, V., Raymond, C., Retta, R., Riback, M., Riley, R., Rise, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schupbach, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N.,
Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Teste, S.,
Theodore, J., Topham, K., Travers, M., Travers, N., Triggillo, D.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

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TITLE Direct Submission
JOURNAL Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 144000)
Birken, B., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
Barn, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collamore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
Horton, J., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J.,
Mathews, C., McCarthy, M., Meldrum, J., Meneus, L., Mihova, T.,
Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicot, R., Norbu, C.,

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TITLE
JOURNAL
REFERENCE
AUTHORS

Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Testfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (16-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 144000)

Birren, B., Nusbaum, C., Lander, E., Abouelella, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeAtellano, K., Dier, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melgrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramsamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (26-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

5 (bases 1 to 144000)

Birren, B., Nusbaum, C., Lander, E., Abouelella, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeAtellano, K., Dier, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kelle, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melgrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramsamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (11-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Mar 11, 2003 this sequence version replaced g127902327.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: 127277
Center clone name: 784_N_20

Only the first 144,000 kilobases of this clone are being submitted.

FEATURES
source
The remainder overlaps accession number AC124319 [MIGR project 127275].

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RESULT 9
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VERSION AC015559.10 GI:13173726
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS FULLTOP.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
1 (bases 1 to 187865)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

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AUTHORS
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Fedeerspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Lam,B., Marathe,R., Miranda,M., Morehouse,A.U., Nguyen,M.,
Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmy,J.,
Yu,S. and Davis,R.W.

```

```

JOURNAL
Unpublished
2 (bases 1 to 187865)
Bruno,D., Conn,L., Dela Rosa,M., Fedeerspiel,N., Foreman,P.,
Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
Morehouse,A.U., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
Yu,S. and Davis,R.W.

```

```

TITLE
Direct Submission
JOURNAL
Submitted (17-NOV-1999) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

```

```

COMMENT
On Mar 1, 2001 this sequence version replaced gi:11968315.
----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center

```

```

Center code: SDBSTD
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
----- Project Information
Center project name: RP11-334C17

```

```

----- Summary Statistics
Sequencing Vector: M13mp18; X02513
Chemistry: Dye-terminator Big Dye; 89% of reads
Assembly program: Phrap; version 0.990319

```

Consensus quality: 180520 bases at least Q40
 Consensus quality: 18182 bases at least Q30
 Consensus quality: 182303 bases at least Q20
 Insert size: 190560; agarose-fp
 Insert size: 186865; sum-of-contigs
 Quality coverage: 9.0x in Q20 bases; sum-of-contigs.
 Quality coverage: 9.2x in Q20 bases; sum-of-contigs.
 NOTE: This is a 'working draft' sequence. It currently
 consists of 11 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 3078: contig of 3078 bp in length
 * 3079 3178: gap of unknown length
 * 3179 6672: contig of 3494 bp in length
 * 6673 6772: gap of unknown length
 * 6773 10097: contig of 3325 bp in length
 * 10098 10197: gap of unknown length
 * 10198 15387: contig of 5190 bp in length
 * 15388 15487: gap of unknown length
 * 15488 24378: contig of 8891 bp in length
 * 24379 24479: gap of unknown length
 * 24479 34707: contig of 10229 bp in length
 * 34708 34807: gap of unknown length
 * 34808 46757: contig of 11949 bp in length
 * 46757 46856: gap of unknown length
 * 46857 67497: contig of 20641 bp in length
 * 67498 67597: gap of unknown length
 * 67598 91511: contig of 23914 bp in length
 * 91512 91611: gap of unknown length
 * 91612 118431: contig of 26820 bp in length
 * 118432 118532: gap of unknown length
 * 118532 187865: contig of 69334 bp in length.

FEATURES

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 /note="assembly_name:Contig38"
 misc_feature
 67598..91511
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 misc_feature
 91612..118431
 /note="assembly_name:Contig40"
 misc_feature
 118532..187865
 /note="assembly_name:Contig41"

ORIGIN

Query Match 50.8%; Score 212; DB 2; Length 187865;
 Best Local Similarity 100.0%; Pred. No. 1,4e-98;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGGGAAGTCTGCGCGAGGAGTCTCGCACTACGCGACTGACGAGAGACTGTGG 60
 Db 73791 ATGGGGGAAGTCTGCGCGAGGAGTCTCGCACTACGCGACTGACGAGAGACTGTGG 73850
 Qy 61 GAGTATATGAGAGACCAACCGCCACAGATGTGTATCTGTGATCTTCCCCACCGCTTACC 120
 Db 73851 GAGTATATGAGAGACCAACCGCCACAGATGTGTATCTGTGATCTTCCCCACCGCTTACC 73910
 Qy 121 CCCATCTGGCGCGAGGCGCAAGGTGCTGTGCGAGCTGACGAGAGAGAGTGTCTCAGAC 180
 Db 73911 CCCATCTGGCGCGAGGCGCAAGGTGCTGTGCGAGCTGACGAGAGAGAGTGTCTCAGAC 73970
 Qy 181 CCCGCGCTCACCAACAGCGCCATCGCGGCGG 212
 Db 73971 CCCGCGCTCACCAACAGCGCCATCGCGGCGG 74002

RESULT 10

AC109321
 LOCUS

DEFINITION Homo sapiens chromosome 17 clone RP11-1079610 map 17, 5 unordered
 pieces.

ACCESSION

AC109321.15
 VERSION

KEYWORDS

HTG; HTGS PHASE1; HTGS_FULLTOP; HTGS_CANCELLED.

SOURCE

Homo sapiens
 (human)

REFERENCE

1 (bases 1 to 207822)
 Birren, B., Nussbaum, C. and Lander, E.
 Homo sapiens chromosome 17, clone RP11-1079610

AUTHORS

Unpublished

JOURNAL

Unpublished

REFERENCE

Unpublished

AUTHORS

Unpublished

Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,
 Anderson, S., Berra, N., Baetien, V., Boguslavsky, L., Boukhalter, B.,
 Brown, A., Camarata, V., Campopiano, A., Chang, J., Chazaro, B.,
 Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
 Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S.,
 Ferreira, P., Fitzhugh, W., Gage, D., Galaean, J., Gardyna, S.,
 Glade, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kamat, A., Karatae, A., Kells, C., Lacroque, K., Lamarca, R.,
 Lander, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C.,
 MacDonald, P., Major, J., Marguis, N., Matthews, C., McCarthy, M.,
 McEwan, P., McKernan, K., Meidrim, J., Menus, L., Mihova, T.,
 Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
 Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
 Peterson, K., Phunkhang, P., Plerie, N., Polara, V., Raymond, C.,
 Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
 Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S.,
 Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J.,
 Topnam, K., Travers, W., Travis, N., Triggillo, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

Direct Submission

JOURNAL

Submitted (03-FEB-2002)

REFERENCE

Submitted (03-FEB-2002)

AUTHORS

Submitted (03-FEB-2002)

Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 207822)
 Birren, B., Nussbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
 Berra, N., Baetien, V., Bloom, T., Boguslavsky, L., Boukhalter, B.,
 Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
 Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
 Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galaean, J.,
 Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B.,
 Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kamat, A., Karatae, A., Kells, C., Lacroque, K., Lamarca, R.,
 Lander, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C.,
 MacDonald, P., Major, J., Marguis, N., Matthews, C., McCarthy, M.,
 McEwan, P., McKernan, K., Meidrim, J., Menus, L., Mihova, T.,
 Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
 Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
 Peterson, K., Phunkhang, P., Plerie, N., Polara, V., Raymond, C.,
 Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
 Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S.,
 Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J.,
 Topnam, K., Travers, W., Travis, N., Triggillo, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

* 6200 6299: gap of 100 bp
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* 6970 7066: gap of 100 bp
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* 7870 7879: gap of 100 bp
* 7880 8568: contig of 689 bp in length
* 8569 8568: gap of 100 bp
* 9365 9364: contig of 696 bp in length
* 9465 9464: gap of 100 bp
* 10171 10171: contig of 707 bp in length
* 10172 10271: gap of 100 bp
* 10272 10963: contig of 692 bp in length
* 10964 11063: gap of 100 bp
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* 14099 14198: gap of 100 bp
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* 21214 21313: gap of 100 bp
* 21314 21988: contig of 675 bp in length
* 21989 22081: gap of 100 bp
* 22082 22801: contig of 713 bp in length
* 22803 22901: gap of 100 bp
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* 24356 24455: gap of 100 bp
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* 25147 25246: gap of 100 bp
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* 30813 31504: contig of 692 bp in length
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* 47365 48069: contig of 705 bp in length
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* 49737 50437: contig of 701 bp in length
* 50438 50538: gap of 100 bp
* 50539 51213: contig of 676 bp in length
* 51214 51313: gap of 100 bp
* 51314 51999: contig of 666 bp in length
* 52000 52099: gap of 100 bp
* 52099 52792: contig of 693 bp in length
* 52793 52892: gap of 100 bp
* 52893 53594: contig of 702 bp in length
* 53595 53694: gap of 100 bp
* 53695 54377: contig of 683 bp in length
* 54378 54477: gap of 100 bp
* 54478 55173: contig of 696 bp in length.

FEATURES
source location/Qualifiers
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Query Match 49.2%; Score 205; DB 2; Length 55173;
Best Local Similarity 100.0%; Pred. No. 6.9e-95;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20167 GGGCACTTCTGATTTGCTGAAGACTGAGGGAAGAACGGGGCCATGCGCTTCTGAG 20108

QY 271 AGCGTAATTCCACAACCTGAGCTTACACCCCTGTCACCGGCTGAGCTGATGTT 330
Db 20107 AGCGTAATTCCACAACCTGAGCTTACACCCCTGTCACCGGCTGAGCTGATGTT 20048

QY 331 GACTTCACTTATGAGCGTGAGAGCTTCGACTTTGACGGTTTGACAGGCACTTCTAG 390
Db 20047 GACTTCACTTATGAGCGTGAGAGCTTCGACTTTGACGGTTTGACAGGCACTTCTAG 19988

QY 391 AACCTCAGGCTCTGTGTAACCCAG 415
Db 19987 AACCTCAGGCTCTGTGTAACCCAG 19963

RESULT 12
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LOCUS
DEFINITION
AC137736 74301 bp DNA linear HMG 28-NOV-2002
Homo sapiens chromosome 17 clone RP13-365D24 map 17, LOW-PASS
SEQUENCE SAMPLING.
AC137736
AC137736.1 GI:25815500
HMG; HTGS_PHASE0.
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 74301)
Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone RP13-365D24
2 (bases 1 to 74301)
Unpublished
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
AC137736
Barnett, B., Bustin, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Camata, J., Chang, J., Chazaro, B., Choquet, Y., Collymore, A.,
Cook, A., Cooke, P., Dearlano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J.,
Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N.,
Hagoe, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J.,
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Ming, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., North, C.,
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retz, R.,
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Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Toham, K.,
Travers, M., Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (28-NOV-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02144, USA
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L28728
Center clone name: 365_D_24

* NOTE: This record contains 91 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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* 1
* 707: contig of 707 bp in length
* 708
* 807: gap of 100 bp
* 808
* 1540: contig of 733 bp in length
* 1541
* 1640: gap of 100 bp
* 1641
* 2344: contig of 704 bp in length
* 2345
* 2444: gap of 100 bp
* 2445
* 3156: contig of 712 bp in length
* 3157
* 3256: gap of 100 bp
* 3257
* 3978: contig of 722 bp in length
* 3979
* 4078: gap of 100 bp

4079
4782
4882
5594
5595
5694
5695
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6406
6506
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7198
7298
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8115
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33439
34162
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4881: gap of 100 bp
5594: contig of 713 bp in length
5694: gap of 100 bp
6405: contig of 711 bp in length
6406: gap of 100 bp
7197: contig of 692 bp in length
7198: gap of 100 bp
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8919: contig of 735 bp in length
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10454: contig of 701 bp in length
10554: gap of 100 bp
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17817: contig of 711 bp in length
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17918: gap of 100 bp
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18742: gap of 100 bp
19458: contig of 716 bp in length
19558: gap of 100 bp
20264: contig of 706 bp in length
20364: gap of 100 bp
20365: contig of 733 bp in length
21103: contig of 733 bp in length
21104: gap of 100 bp
21203: gap of 100 bp
21910: contig of 707 bp in length
21911: gap of 100 bp
22010: gap of 100 bp
22731: contig of 721 bp in length
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23556: contig of 725 bp in length
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24373: contig of 717 bp in length
24473: gap of 100 bp
25166: contig of 693 bp in length
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25267: gap of 100 bp
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26763: contig of 714 bp in length
26764: gap of 100 bp
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27583: contig of 720 bp in length
27584: gap of 100 bp
27684: gap of 100 bp
28421: contig of 738 bp in length
28422: gap of 100 bp
28522: contig of 702 bp in length
29224: gap of 100 bp
29324: gap of 100 bp
30031: contig of 708 bp in length
30032: gap of 100 bp
30132: gap of 100 bp
30859: contig of 728 bp in length
30860: gap of 100 bp
30960: gap of 100 bp
31693: contig of 734 bp in length
31694: gap of 100 bp
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32516: gap of 100 bp
32517: gap of 100 bp
32617: contig of 722 bp in length
33338: gap of 100 bp
33438: gap of 100 bp
34162: contig of 724 bp in length

LOCUS	3995 bp	RNA	linear	ROD 07-OCT-2003
DEFINITION	BC029102	Mus musculus caspase recruitment domain family, member 14, mRNA		
ACCESSION	BC029102	(CDNA clone MGC:28122 IMAGE:3579883), complete cds.		
VERSION	BC029102.1	GI:22137687		
KEYWORDS	MGC.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	1 (bases 1 to 3995)			
AUTHORS	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Ditchken L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Steplton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaez T.E., Brownstein M.J., Udell T.B., Toobyakki S., Carninci P., Prange C., Raha S.S., Loquiano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McCorman K.J., Malek J.A., Gunaratne P.H., Richards S., Woley K.C., Hale S., Garcia A.M., Gay L.U., Hily S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Searched A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S., Krzywinski M.I., Skalka J., Smalhus D.E., Scherch A., Schein J.E., Jones S.J. and Marra M.A.			
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
MEDLINE	22388257			
PUBMED	12477932			
REFERENCE	2 (bases 1 to 3995)			
AUTHORS	Strausberg R.			
TITLE	Direct Submission			
JOURNAL	Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov			
COMMENT	Contact: MGC help desk Email: cgapbs-rc@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNML) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amg@bcm.tmc.edu Gunaratne, P.H., Garcia, A.M., Lu, X., Hily, S.W., Louisseged, H., Kwon, C.R., Sneed, A.J., Martin, R.G., Muzny, D.W., Navevati, A.N., Gibbs, R.A.			
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNML at: http://image.llnl.gov Series: IRAX Plate: 36 Row: e Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 18700027			
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    at their amino terminus. This family represents the rest
    of these proteins"
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    /note="PBD; Region: Domain present in PBD-95, Dlg, and
    ZO-1/2. Also called DHR (Dlg homologous region) or GUSP
    (relatively well conserved tetrapeptide in these domains).
    Some PDzs have been shown to bind C-terminal polypeptides"
    /db_xref="CDD:smart00228"

misc_feature
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    (relatively well conserved tetrapeptide in these domains).
    Some PDzs have been shown to bind C-terminal polypeptides"
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Query Match 7.9%; Score 33; DB 10; Length 3995;
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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 CTCACCCCTTACTCTGCGCCGACGCAAGTCTG 147
Db 439 CTCACCCCTTACTCTGCGCCGACGCAAGTCTG 471

RESULT 15
LOCUS AL645911 244653 bp DNA linear ROD 09-AUG-2002
DEFINITION Mouse DNA sequence from clone RP23-25M3 on chromosome 11, complete
sequence.
ACCESSION AL645911
VERSION AL645911.14 GI:22204307
KEYWORDS HMG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Molecular Systematics: Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 244653)
AUTHORS Tromans,A.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humuery@sanger.ac.uk
COMMENT humuery@sanger.ac.uk
On Aug 11, 2002 this sequence version replaced gi:21531055.
----- Genome Center

```


Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk

 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-25M3 is from the RP23-25 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBAC3.6.

FEATURES

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 /db_xref="taxon:10090"
 /chromosome="11"
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Best Local Similarity 100.0%; Pred. No. 5.6e-06; Indels 0; Gaps 0;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: March 22, 2004, 01:25:26
 Job time : 3004 secs


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FT      exon      3139..3417
FT      /*tag= v
FT      /number= 21
XX      WO200159065-A2.
XX      16-AUG-2001.
XX      22-JAN-2001; 2001WO-US002087.
XX      09-FEB-2000; 2000US-0181159P.
XX      (MILL-) MILLENNIUM PHARM INC.
XX      Bertin J;
XX      WPI; 2001-497073/54.
XX      P-PSDB; AAE07165.
XX      An isolated caspase recruitment domain polypeptide useful for regulating
XX      growth and cell death and useful for the treatment of cancer.
XX      Disclosure; Fig 2A-2C; 109pp; English.
XX      The present sequence is human caspase recruitment domain-14 (CARD-14)
XX      DNA. The CARD-14 gene is located on chromosome 17. The CARD-14 is used
XX      for the detection of modulators that modulates the ability of CARD-14 to
XX      bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation of
XX      nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating
XX      growth and cell death and useful for the treatment of cancer. It is also
XX      useful for the treatment of autoimmune disorders (e.g., systemic lupus
XX      erythematosus), neurological disorders (e.g., Alzheimer's and Parkinson's
XX      disease), inflammatory disorders, haematological disorders (e.g., anaemia,
XX      myelodysplastic syndromes), myocardial infarctions, strokes, immune
XX      disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling
XX      disorders and certain viral and bacterial infections
XX      Sequence 3417 BP; 739 A; 1039 C; 1102 G; 537 T; 0 U; 0 Other;
XX      Query Match 99.5%; Score 415; DB 4; Length 3417;
XX      Best Local Similarity 100.0%; Pred. No. 1e-196;
XX      Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      301 ACCCTGTCACCGGGGCTGCAGGCGCTGATGTTGACTTCACTTAAGCTTACGGGTGAGAGCTCC 360
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DB      361 GACTTTGACGGGTTTGCGAGGCACTTTAGAAACCTGAGGCTCTGTGTAACCCAG 415
XX      RESULT 3
XX      ADB62161
XX      ID ADB62161 standard; cDNA; 3766 BP.
XX      AC ADB62161;
XX      DT 04-DEC-2003 (first entry)
XX      DE Human cDNA encoding clone CTONG20007660.
XX      KW Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
XX      KW tissue regeneration; cell regeneration; membrane protein;
XX      KW signal transduction-related protein; transcription-related protein;
XX      KW osteoporosis; neurological disease; cancer; tumour.
XX      OS Homo sapiens.
XX      FH Key Location/Qualifiers
XX      FT CDS 192..1448
XX      FT /*tag= a
XX      FT /product= "Clone CTONG20007660 protein"
XX      PN EP1308459-A2.
XX      PD 07-MAY-2003.
XX      PF 28-MAR-2002; 2002EP-00007401.
XX      PR 05-NOV-2001; 2001EP-00379298.
XX      PR 25-JAN-2002; 2002US-00350978.
XX      PA (HELI-) HELIX RES INST.
XX      PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX      PI Iosogi T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX      PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX      PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
XX      DR WPI; 2003-450961/43.
XX      DR P-PSDB; ADB64131.
XX      PT New polynucleotides and polypeptides, useful for developing a diagnostic
XX      marker or medicines for regulation of their expression and activity, or
XX      PT as targets of gene therapy.
XX      PS Claim 1; Page; 222pp; English.
XX      The invention discloses a polynucleotide comprising a sequence selected
XX      from 1970 fully defined nucleotide sequences which encode novel
XX      polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
XX      or its partial peptide, an antibody binding to the polypeptide or peptide
XX      of the polynucleotide, immunologically assaying the polypeptide or
XX      peptide of the polynucleotide by contacting the polypeptide or peptide
XX      with the antibody of the encoded protein, and observing the binding
XX      between the two, a transformant carrying the polynucleotide in an
XX      expressible manner and an antisense polynucleotide. The oligonucleotide
XX      is useful as a primer for synthesising the polynucleotide, or as a probe
XX      for detecting the polynucleotide. The polynucleotides and encoded
XX      proteins are useful as pharmaceutical agents and many disease-related
XX      genes may be included in them, for developing a diagnostic marker or
XX      medicines for regulation of their expression and activity, or as targets
XX      of gene therapy. The genes are involved in tissue and/or cell
XX      regeneration. Membrane proteins, signal transduction-related proteins,
XX      transcription-related proteins, disease-related proteins and genes
XX      encoding them can be used as indicators for diseases (e.g. osteoporosis,
XX      neurological diseases, cancer, tumours. The cDNA may be used to regulate

```

CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a cDNA of the invention. Note: Some of the sequence
CC data for this patent is not represented in the printed specification, but
CC is based on sequence information supplied by the European Patent Office.

XX Sequence 3766 BP; 764 A; 1140 C; 1217 G; 645 T; 0 U; 0 Other;

Query Match 84.2%; Score 351; DB 9; Length 3766;
Best Local Similarity 100.0%; Pred. No. 8.2e-165;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGAATCTGTGCGCCAGGAGACTCCGCACTACAGGCACTGACAGAGACACTGTGG 60
DB 192 ATGGGGGAATCTGTGCGCCAGGAGACTCCGCACTACAGGCACTGACAGAGACACTGTGG 251
QY 61 GAGATGATGAGAGAGCCAGGCAAGGATGTAAGCTGATCCGCCAGCCGCTCACC 120
DB 252 GAGATGATGAGAGAGCCAGGCAAGGATGTAAGCTGATCCGCCAGCCGCTCACC 311
QY 121 CCTTACTGCGCCAGGCAAGGATGTAAGCTGATCCGCCAGGAGAGAGTGTGCACAGC 180
DB 312 CCTTACTGCGCCAGGCAAGGATGTAAGCTGATCCGCCAGGAGAGAGTGTGCACAGC 371
QY 181 CCGCGGCTCACCAACAGCGGCATGCGGGCCGCGCACTGCTGATTTGCTGAAGACTCGA 240
DB 372 CCGCGGCTCACCAACAGCGGCATGCGGGCCGCGCACTGCTGATTTGCTGAAGACTCGA 431
QY 241 GGGAGAAAGCGGGCGCATGCGCTTCTGAGAGAGCTGAAAGTTCCAAACCTGACGCTTAC 300
DB 432 GGGAGAAAGCGGGCGCATGCGCTTCTGAGAGAGCTGAAAGTTCCAAACCTGACGCTTAC 491
QY 301 ACCCTGTGTCACCGGGCTGACGCGTGAATGTTAGCTTCACTTAATTTAGCGGT 351
DB 492 ACCCTGTGTCACCGGGCTGACGCGTGAATGTTAGCTTCACTTAATTTAGCGGT 542

RESULT 4

ID AAD13447 standard; cDNA; 3931 BP.

XX AAD13447;

DT 06-NOV-2001 (first entry)

DE Human caspase recruitment domain-14 (CARD-14) cDNA.

XX Human; caspase recruitment domain-14; CARD-14; chromosome 17;
KW nuclear factor-kappa B; NF-kB; cell growth; cell death; cancer; therapy;
KW autoimmune disorder; systemic lupus erythematosus; neurological disorder;
KW Alzheimer's disease; Parkinson's disease; inflammatory disorder; anaemia;
KW haematological disorder; myelodysplastic syndrome; myocardial infarction;
KW stroke; immune disorder; Crohn's disease; allergic rhinitis; infection;
KW cell signalling disorder; cytoskeletal; immunosuppressive; motropic;
KW neuroprotective; antiviral; antibacterial; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
XX CDS 207..3221

FT //tag= a
FT /product= "Human caspase recruitment domain-14"
FT /note= "Residues 207-3218 is specifically claimed as SEQ
ID NO 3 in claim 9 of the specification"

XX WO200159065-A2.

PD 16-AUG-2001.

PF 22-JAN-2001; 2001WO-US002087.

PR 09-FEB-2000; 2000US-0181159P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Bertin U;
PI WPI; 2001-497073/54.
DR P-PsDB; AAB07164.

PT An isolated caspase recruitment domain polypeptide useful for regulating
PT growth and cell death and useful for the treatment of cancer.
PS Claim 9; Fig 1A-1E; 109pp; English.

CC The present sequence is human caspase recruitment domain-14 (CARD-14)
CC cDNA. The CARD-14 gene is located on chromosome 17. The CARD-14 is used
CC for the detection of modulators that modulates the ability of CARD-14 to
CC bind to Bcl-10 and stimulates phosphorylation of Bcl-10 or activation of
CC nuclear factor-kappa B (NF-kB). The CARD-14 is useful for regulating
CC growth and cell death and useful for the treatment of cancer. It is also
CC useful for the treatment of autoimmune disorders (e.g., systemic lupus
CC erythematosus), neurological disorders (e.g., Alzheimer's and Parkinson's
CC disease, inflammatory disorders, haematological disorders (e.g., anaemia,
CC myelodysplastic syndromes), myocardial infarctions, strokes, immune
CC disorders (e.g., Crohn's disease, allergic rhinitis), cell signalling
CC disorders and certain viral and bacterial infections

SQ Sequence 3931 BP; 799 A; 1187 C; 1263 G; 682 T; 0 U; 0 Other;

Query Match 84.2%; Score 351; DB 4; Length 3931;
Best Local Similarity 100.0%; Pred. No. 8.1e-165;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGAATCTGTGCGCCAGGAGACTCCGCACTACAGGCACTGACAGAGACACTGTGG 60
DB 207 ATGGGGGAATCTGTGCGCCAGGAGACTCCGCACTACAGGCACTGACAGAGACACTGTGG 266
QY 61 GAGATGATGAGAGAGCCAGGCAAGGATGTAAGCTGATCCGCCAGCCGCTCACC 120
DB 267 GAGATGATGAGAGAGCCAGGCAAGGATGTAAGCTGATCCGCCAGCCGCTCACC 326
QY 121 CCTTACTGCGCCAGGCAAGGATGTAAGCTGATCCGCCAGGAGAGAGTGTGCACAGC 180
DB 327 CCTTACTGCGCCAGGCAAGGATGTAAGCTGATCCGCCAGGAGAGAGTGTGCACAGC 386
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DB 387 CCGCGGCTCACCAACAGCGGCATGCGGGCCGCGCACTGCTGATTTGCTGAAGACTCGA 446
QY 241 GGGAGAAAGCGGGCGCATGCGCTTCTGAGAGAGCTGAAAGTTCCAAACCTGACGCTTAC 300
DB 447 GGGAGAAAGCGGGCGCATGCGCTTCTGAGAGAGCTGAAAGTTCCAAACCTGACGCTTAC 506
QY 301 ACCCTGTGTCACCGGGCTGACGCGTGAATGTTAGCTTCACTTAATTTAGCGGT 351
DB 507 ACCCTGTGTCACCGGGCTGACGCGTGAATGTTAGCTTCACTTAATTTAGCGGT 557

RESULT 5

ID ABX11449 standard; cDNA; 1141 BP.

XX ABX11449;

DT 09-MAY-2003 (first entry)

DE Human CARD-12X expressed sequence tag, GI10316320.

XX Human; ss; CARD; EST; caspase recruitment domain; apoptosis; lupus;
KW cell adhesion; inflammation; cytokine receptor signalling; glioma;
KW carcinoma; adenocarcinoma; hamartoma; leukaemia; lymphoma; melanoma;
KW CARD-containing polypeptide associated disorder; sarcoma; neoplasia;
KW keratinocyte hyperplasia; keloid; benign prostatic hypertrophy; sepsis;
KW inflammatory hyperplasia; fibrosis; restenosis; allergy; arthritis;
KW Sjogren's syndrome; Crohn's disease; ulcerative colitis; stroke; cancer;
KW graft versus host disease; abnormal cell death disease; heart failure;

KW myocardial infarction; neurodegenerative disease; Parkinson's disease;
KM Alzheimer's disease; HIV; CARD-12X; caspase activator; caspase inhibitor;
XX expressed sequence tag.
XX
XX Homo sapiens.
XX OS
XX PN US2002164703-A1.
XX PD
XX PF 07-NOV-2002.
XX PP 19-DEC-2001; 2001US-00032159.
XX PR 21-DEC-2000; 2000US-0257457P.
XX PA (PAML/) PAWLOWSKI K.
XX PA (REED/) REED J C.
XX PA (GODZ/) GODZIK A.
XX PI Pawlowski K, Reed JC, Godzik A;
XX DR WPI; 2003-288137/28.
XX PT New isolated CARD-containing nucleic acids, useful for the diagnosis and
XX PT treatment of disorders with aberrant expression or activity of the CARD-
XX PT containing polypeptide, such as cancer, stroke, arthritis, heart failure
XX PT and AIDS.
XX PS Disclosure: Fig 7; 34pp; English.
XX
XX CC The invention relates to an isolated nucleic acid molecule encoding a
XX CC caspase recruitment domain (CARD) containing polypeptide. CARD containing
XX CC polypeptides are involved in apoptosis (as caspase activators and caspase
XX CC inhibitors), cell adhesion, inflammation and cytokine receptor
XX CC signalling. The methods and compositions of the present invention are
XX CC useful for the diagnosis and treatment of disorders associated with the
XX CC aberrant expression or activity of the CARD containing polypeptide such
XX CC as cancer, glioma, carcinoma, adenocarcinoma, sarcoma, melanoma, keloid,
XX CC hamartoma, leukæmia, lymphoma, keratinocyte hyperplasia, neoplasia,
XX CC benign prostatic hypertrophy, inflammatory hyperplasia, fibrosis,
XX CC resectosis, allergies, inflammatory diseases such as arthritis, lupus,
XX CC Sjogren's syndrome, Crohn's disease, ulcerative colitis, graft versus
XX CC host disease, sepsis, abnormal cell death diseases such as stroke,
XX CC myocardial infarction, heart failure, neurodegenerative diseases like
XX CC Parkinson's disease and Alzheimer's disease, and HIV infection. The
XX CC present sequence represents the human caspase recruitment domain
XX CC containing protein, CARD-12X expressed sequence tag, GI10316320
XX
XX SQ Sequence 1141 BP; 318 A; 351 C; 320 G; 152 T; 0 U; 0 Other;
XX
XX Query Match 26.4%; Score 110; DB 7; Length 1141;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-44;
XX Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1 ATGGGGGAACTGTCGGAGGAGCTCCGACCTCAGCGACTGAGAGAGACACTGTGG 60
XX DB 161 ATGGGGGAACTGTCGGAGGAGCTCCGACCTCAGCGACTGAGAGAGACACTGTGG 220
XX
XX QY 61 GAGATGATGAGAGAGCCACCGCCACAGATGATGATGATGATGATGATGATGATGAT 110
XX DB 221 GAGATGATGAGAGAGCCACCGCCACAGATGATGATGATGATGATGATGATGATGAT 270
XX
XX RESULT 6
XX ACA38053
XX ID ACA38053 standard; DNA; 534 BP.
XX AC ACA38053;
XX DT 19-JUN-2003 (first entry)
XX DE Prokaryotic essential gene #19710.
XX KW Antisense; ds; prokaryotic essential gene; cell proliferation;

KW drug design; gene.
XX
XX OS Mycobacterium avium.
XX PN WO20027183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KU, Zykkind JW;
XX PI Mail D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR P-PSDB; ABU34183.
XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX
XX PS Claim 14; SEQ ID NO 25923; 1766pp; English.
XX
XX CC The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC polypeptide or its fragment whose expression is inhibited by the
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX CC proliferation or the activity of a gene in an operon required for
XX CC proliferation; (7) identifying a compound that influences the activity of
XX CC the gene product or that has an activity against a biological pathway
XX CC required for proliferation, or that inhibits cellular proliferation; (8)
XX CC identifying a gene required for cellular proliferation or the biological
XX CC pathway in which a proliferation-required gene or its gene product lies
XX CC or a gene on which the test compound that inhibits proliferation of an
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX CC compound's activity; (11) a culture comprising strains in which the gene
XX CC product is overexpressed or underexpressed; (12) determining the extent
XX CC to which each of the strains is present in a culture or collection of
XX CC strains; or (13) identifying the target of a compound that inhibits the
XX CC proliferation of an organism. The antisense nucleic acids are useful for
XX CC identifying proteins or screening for homologous nucleic acids required
XX CC for cellular proliferation to isolate candidate molecules for rational
XX CC drug discovery programs, or for screening homologous nucleic acids
XX CC required for proliferation in cells other than S. aureus, S. typhimurium,
XX CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
XX CC prokaryotic essential genes. Note: The sequence data for this patent did
XX CC not form part of the printed specification, but was obtained in
XX CC electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 534 BP; 98 A; 187 C; 166 G; 83 T; 0 U; 0 Other;
XX
XX Query Match 4.8%; Score 20; DB 7; Length 534;
XX Best Local Similarity 100.0%; Pred. No. 9.6;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 305 TGGTCAACCGGGCTGACGCT 324
XX DB 290 TGGTCAACCGGGCTGACGCT 309

RESULT 7

ABN20134/c

ID ABN20134 standard; cDNA; 550 BP.

XX ABN20134;

XX 24-JUN-2002 (first entry)

XX Human ORFX polynucleotide sequence SEQ ID NO:8745.

XX Human, open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypochyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis; gene; ss.

XX Homo sapiens.

XX PN WO200192523-A2.

XX PD 06-DEC-2001.

XX PF 29-MAY-2001; 2001WO-US010836.

XX PK 30-MAY-2000; 2000US-0206132P.

XX PR 29-AUG-2000; 2000US-0228716P.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach MD;

XX WPI; 2002-106308/14.

XX P-PSDB; ABP04382.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders.

XX PS Disclosure; SEQ ID NO 8745; 1037PP; English.

XX The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see table 1
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences

XX Sequence 550 BP; 177 A; 112 C; 137 G; 124 T; 0 U; 0 Other;

XX Query March 4.6%; Score 19; DB 6; Length 550;

XX Best Local Similarity 100.0%; Pred. No. 30;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 GGAGCACTGTGGAGATG 66

DB 258 GGAGCACTGTGGAGATG 240

RESULT 8

AAA09358/c

ID AAA09358 standard; DNA; 867 BP.

XX AAA09358;

XX 10-AUG-2000 (first entry)

XX p75-NTR (neurotrophin receptor) extracellular portion DNA.

KW p75 neurotrophin receptor; extracellular; p75-NTR; death receptor;
 KW apoptosis; death signal domain; antagonist; cell survival; cytostatic;
 KW neuroprotective; antiparkinsonian; antidiabetic; anti-HIV; virucide;
 KW neurotrophic; anticonvulsant; cerebroprotective; ss.

XX Rattus sp.

XX Key Location/Qualifiers

XX Mat_peptide 115..867

XX WO200020578-A1.

XX 13-APR-2000.

XX PF 05-OCT-1999; 99WO-AU000860.

XX PR 06-OCT-1998; 98AU-00006353.

XX PR 07-OCT-1998; 98AU-00006351.

XX PR 01-JUN-1999; 99AU-00000701.

XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX Bartlett PF, Coulson EJ, Fieldew K, Baca M, Kilpatrick T;

XX Surindar C;

XX WPI; 2000-328933/28.

XX P-PSDB; AAY92372.

XX Novel nucleic acids encoding a peptide capable of facilitating the death

XX of a cell, useful for antagonizing cell death signal function and

XX promoting cell death, e.g. for treating cancer.

XX Claim 13; Page 71-72; 80PP; English.

XX This DNA encodes the extracellular portion (or ligand binding molecule)
 CC of rat p75 neurotrophin receptor (p75-NTR). p75-NTR is multifunctional
 CC and is capable of acting as a death receptor. Elevated p75-NTR expression
 CC results in increased death in vitro and in vivo. It has been determined
 CC that the death signal is not the cytoplasmic motif known as the death
 CC domain, but is a region adjacent the membrane domain on p75-NTR.
 CC Identification of this region provides an opportunity to modulate cell
 CC survival by antagonizing the death signalling region or promoting the
 CC apoptosis by providing cells with the genetic material to express the
 CC death signalling region adjacent, proximal, or otherwise juxtaposed or
 CC associated membrane of a cell or to express the death signalling region
 CC in multicentric form. The polypeptides and methods of the invention are
 CC useful for inhibiting, reducing or antagonizing p75-NTR-mediated death
 CC signals in neural cells. In particular, the methods are used for the
 CC treatment or prophylaxis of disease conditions associated with neural
 CC death or where cell death is to be promoted such as in treating or
 CC preventing cancer growth and/or development. Other diseases capable of
 CC treatment include neurodegenerative diseases, such as cerebral palsy,
 CC trauma induced paralysis, vascular ischemia associated with stroke,
 CC neural tumors, motorneuron diseases, Parkinson's disease, Huntington's
 CC disease, Alzheimer's disease, multiple sclerosis and peripheral
 CC neuropathies associated with diabetes, heavy metal or alcohol toxicity,

CC renal failure, and/or infectious diseases such as Herpes, rubella,
CC measles, chicken pox, HIV and HTLV-1 (all claimed). The methods are also
CC useful for treating neurons or glia damaged by trauma or disease
CC (claimed). Animals which can be treated include humans, livestock
CC animals, laboratory test animals, companion animals, and captive wild
CC animals
XX
SQ Sequence 867 BP, 177 A, 260 C, 288 G, 142 T, 0 U, 0 Other;
Query Match 4.6%; Score 19; DB 3; Length 867;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 388 AGGAACCTCAGGCTCTGG 406
DB 771 AGGAACCTCAGGCTCTGG 753
RESULT 9
ADB58069/c
ID ADB58069 standard; DNA; 3259 BP.
XX
AC ADB58069;
XX
DT 04-DEC-2003 (first entry)
XX
DE Toxicity-related gene, SEQ ID 3095.
XX
KM Toxic; toxin; gene expression profile; hepatotoxicity; liver;
KM drug screening; toxicity assay; ds.
XX
OS Unidentified.
XX
PN MO2003064624.A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-US003194.
XX
PR 31-JAN-2002; 2002US-00060087.
PR 15-MAR-2002; 2002US-0364045P.
PR 15-MAR-2002; 2002US-0364055P.
PR 30-DEC-2002; 2002US-0436643P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Mendrick D, Porter M, Johnson X, Higgs B, Castle A, Elashoff M;
XX
DR WPI; 2003-689530/65.
XX
XX Predicting a toxic effect of a compound, useful in identifying toxicity
XX makers in liver tissues or cells for drug screening and toxicity assays,
XX comprises preparing gene expression profile of tissue or cells exposed to
XX the compound.
XX
PS Claim 1; SEQ ID NO 3095; 1156pp; English.
XX
XX The present invention relates to a method for predicting a toxic effect
XX of a compound. The method comprises preparing a gene expression profile
XX of a tissue or cell sample exposed to the compound, and comparing the
XX gene expression profile to a database comprising SEQ ID 1-4925, where
XX differential expression of the gene indicates at least one toxic effect.
XX The method is useful for predicting at least one toxic effect of a
XX compound, predicting hepatotoxicity or the progression of a toxic effect
XX of a compound, identifying an agent that modulates the onset or
XX progression of a toxic response, predicting the cellular pathways that a
XX compound modulates in a cell, and identifying an agent that modulates at
XX least one activity of a protein. The method and compositions of the
XX present invention using a database of genes having liver toxin-induced
XX differential expression, are useful in identifying toxicity markers in
XX liver tissues or cells for drug screening and toxicity assays. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3259 BP, 717 A, 976 C, 913 G, 653 T, 0 U, 0 Other;
XX
Query Match 4.6%; Score 19; DB 9; Length 3259;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 388 AGGAACCTCAGGCTCTGG 406
DB 770 AGGAACCTCAGGCTCTGG 752
RESULT 10
AAA09356/c
ID AAA09356 standard; cDNA; 3260 BP.
XX
AC AAA09356;
XX
DT 10-AUG-2000 (first entry)
XX
DE p75-NTR (neurotrophin receptor) coding sequence.
XX
KM p75 neurotrophin receptor; p75-NTR; death receptor; apoptosis;
KM death signal domain; antagonist; cell survival; cyostatic;
KM neuroprotective; antiparkinsonian; antidiabetic; anti-HIV; virucide;
KM neurotropic; anticonvulsant; cerebroprotective; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT 115..1392
XX FT CDS /*tag= a
XX
XX MO200020578-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-AU000860.
XX
PR 06-OCT-1998; 98AU-00006353.
PR 07-OCT-1998; 98AU-00006351.
PR 01-JUN-1999; 99AU-00000701.
XX
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
PI Bartlett PF, Coulson EJ, Fieldew K, Baca M, Kilpatrick T;
PI Surrindar C;
XX
DR WPI; 2000-328933/28.
DR P-PSDB; AA92370.
XX
XX Novel nucleic acids encoding a peptide capable of facilitating the death
XX of a cell, useful for antagonizing cell death signal function and
XX promoting cell death, e.g. for treating cancer.
XX
PS Claim 9; Page 65-69; 80pp; English.
XX
XX This cDNA encodes human p75 neurotrophin receptor (p75-NTR). p75-NTR is
XX multifunctional and is capable of acting as a death receptor. Elevated
XX p75-NTR expression results in increased death in vitro and in vivo. It
XX has been determined that the death signal is not the cytoplasmic motif
XX known as the death domain, but is a region adjacent the membrane domain
XX on p75-NTR. Identification of this region provides an opportunity to
XX modulate cell survival by antagonizing the death signalling region or
XX promoting apoptosis by providing cells with the genetic material to
XX express the death signalling region adjacent, proximal, or otherwise
XX juxtaposed or associated membrane of a cell or to express the death
XX signalling region in multicytic form. The polypeptides and methods of the
XX invention are useful for inhibiting, reducing or antagonizing p75-NTR-
XX mediated death signals in neural cells. In particular, the methods are
XX used for the treatment or prophylaxis of disease conditions associated
XX with neural death or where cell death is to be promoted such as in

CC treating or preventing cancer growth and/or development. Other diseases
CC capable of treatment include neurodegenerative diseases, such as cerebral
CC palsy, trauma induced paralysis, vascular ischemia associated with
CC stroke, neural tumors, motorneuron diseases, Parkinson's disease,
CC Huntington's disease, Alzheimer's disease, multiple sclerosis and
CC peripheral neuropathies associated with diabetes, heavy metal or alcohol
CC toxicity, renal failure, and/or infectious diseases such as Herpes,
CC rubella, measles, chicken pox, HIV and HTLV-1 (all claimed). The methods
CC are also useful for treating neurons or glia damaged by trauma or disease
CC (claimed). Animals which can be treated include humans, livestock
CC animals, laboratory test animals, companion animals, and captive wild
CC animals

XX SQ Sequence 3260 BP; 718 A; 976 C; 913 G; 653 T; 0 U; 0 Other;

Query Match 4.6%; Score 19; DB 3; Length 3260;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 AGGAACCTCAGGCTCCTGG 406
|||||
Db 771 AGGAACCTCAGGCTCCTGG 753

RESULT 11
AAS98203
ID AAS98203 standard; cDNA; 3948 BP.
XX AAS98203;
AC
DT 12-MAR-2002 (first entry)
XX
XX DNA encoding plakoglobin interacting protein #3.
XX
XX Human; plakoglobin; cytoskeletal; osteopathic; dermatological; cardiac;
XX plakoglobin related disease; skin carcinoma; acantholytic disease;
XX basal cell carcinoma; squamous cell carcinoma; Naxos disease; PCR primer;
XX extramammary Paget's disease; heart disease; skin blistering;
XX subcorneal acantholysis; Grover's disease; Halley-Halley's disease;
XX Darier's disease; ectodermal dysplasia; skin fragility syndrome; ss.
XX
XX Homo sapiens.
XX
XX WO200185933-A2.
XX
XX 15-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-EP04872.
XX
XX 09-MAY-2000; 2000EP-00201668.
XX
XX (VLAAs-) VLAAS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
XX Van Roy F, Bonne S, Vanlandschoot A;
XX
XX WPI; 2002-062246/08.
XX
XX P-PSDB; AAU73247.
XX
XX New polypeptide, useful for treating skin carcinoma or acantholytic
XX disease such as Grover's and Darier's disease, comprises a protein
XX interacting with human plakoglobin and involved in transduction of
XX plakoglobin related signal to nucleus.
XX
XX Claim 7; Fig 3; 98pp; English.

CC The invention relates to an isolated plakoglobin interacting polypeptide
CC (I). (I) is useful as a medicament and in the manufacture of a medicament
CC for treating plakoglobin related diseases, such as skin carcinoma or an
CC acantholytic disease, and to screen compounds that interfere with the
CC interaction of the polypeptide with plakoglobin. The plakoglobin related
CC diseases include basal cell carcinoma, squamous cell carcinoma,
CC extramammary Paget's disease, Naxos disease, heart diseases, skin
CC blistering and acantholytic diseases such as subcorneal acantholysis,

CC Grover's disease, Halley-Halley's disease or Darier's disease, and
CC ectodermal dysplasia/skin fragility syndrome. AAS98201- AAS98288
CC represent novel human plakoglobin interacting protein coding sequences
CC and PCR primers of the invention

XX SQ Sequence 3948 BP; 717 A; 1218 C; 1327 G; 686 T; 0 U; 0 Other;

Query Match 4.6%; Score 19; DB 6; Length 3948;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 GGACGAGGAGGAGGCTGCTG 174
|||||
Db 224 GGACGAGGAGGAGGCTGCTG 242

RESULT 12
AAS05388
ID AAS05388 standard; cDNA; 3949 BP.
XX AAS05388;
AC
XX
DT 12-SEP-2001 (first entry)
XX
XX Human caspase recruitment domain, CARD-10 cDNA sequence.
XX
XX Human; caspase recruitment domain; CARD-10; Bcl-10; NF-kappaB; apoptosis;
XX hyperproliferative disorder; autoimmune; neurological;
XX inflammatory disorder; viral infection; stress-related response; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 41..3139
XX FT /tag= a
XX FT /product= "CARD-10"
XX FT /note= "ORF is specifically claimed"
XX
XX WO200140468-A2.
XX
XX 07-JUN-2001.
XX
XX 01-DEC-2000; 2000WO-US032716.
XX
XX 03-DEC-1999; 99US-0168780P.
XX 18-FEB-2000; 2000US-00507533.
XX 25-FEB-2000; 2000US-00513904.
XX 10-OCT-2000; 2000US-00685791.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Bertin J;
XX
XX WPI; 2001-367809/38.
XX
XX P-PSDB; AAU01206.
XX
XX Novel caspase recruitment domain (CARD) proteins, CARD-9, CARD-10, CARD-
XX 11, useful as targets for therapy, as immunogens, and in screening and
XX detection assays.
XX
XX Claim 2; Fig 10A-10C; 145pp; English.

CC The present sequence encoding for novel human caspase recruitment domain,
CC CARD-10 is isolated from a human skin cDNA library. Also described are
CC novel human sequences for CARD-9 and CARD-11 (AAU01205, AAU01207) and rat
CC CARD-9 (AAU01204). CARD-9, CARD-10 and CARD-11 interact with Bcl-10 which
CC is thought to activate nuclear factor (NF)-kappaB and apoptosis. The
CC sequences of the invention can be used for treating a disorder associated
CC with abnormal levels of apoptosis by modulating the expression or
CC activity of CARD-9, CARD-10, or CARD-11. They can be used for the
CC treatment of hyperproliferative disorders (e.g. cancer), autoimmune
CC disorders (e.g. systemic lupus erythematosus), neurological disorders
CC (e.g. Alzheimer's disease), inflammatory disorders (e.g. Crohn's

CC disease) and viral infection (e.g. HIV). The CARD polypeptide, CC polynucleotide and an antibody which selectively binds to CARD can be used in screening and detection assays (e.g. chromosomal mapping, tissue typing), predictive medicine (prognostic assays, monitoring clinical trials, and therapy (treatment and prophylaxis)). The CARD polypeptide may be used to screen for drugs that bind to and/or modulate it. CARD CC sequences are potential targets for regulating inflammation, cancer, NF- κ B signaling, stress-related response and apoptosis in human CC disease. A host cell containing a polynucleotide encoding CARD can be used to create transgenic animals

XX

CC Sequence 3949 BP; 724 A; 1222 C; 1319 G; 684 T; 0 U; 0 Other;

XX

Query Match 4.6%; Score 19; DB 4; Length 3949;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 GGACGAGGAGGAGGCTGCTG 174

DB 220 GGACGAGGAGGAGGCTGCTG 238

RESULT 13

ABA00333

ID ABA00333 standard; cDNA; 3949 BP.

XX

AC ABA00333;

XX

DT 09-DEC-2002 (first entry)

XX

XX Human CARD-10 cDNA.

XX

Gene; rat; human; caspase recruitment domain; CARD-9; CARD-10; CARD-11; apoptosis; inflammation; cell growth; cell death; lymphocyte activation; cancer; melanoma; autoimmune disease; arthritis; neurological disorder; Alzheimer's disease; ss.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT CDS 41..3139

FT /*tag= a

FT /product= "CARD-10"

XX

XX MO200270652-A2.

XX

XX 12-SEP-2002.

XX

XX 28-FEB-2002; 2002WO-US006147.

XX

XX 02-MAR-2001; 2001US-00798412.

XX

XX (MILL-) MILLENNIUM PHARM INC.

XX

XX Bertin J;

XX

XX WPI; 2002-698749/75.

XX

XX P-PSDB; AAG79554.

XX

PT CARD-9, CARD-10 or CARD-11 polypeptides and polynucleotides, useful for treating disorders associated with inappropriate apoptosis or lymphocyte activation, e.g. cancer.

XX

XX Claim 5; Fig 10; 151pp; English.

XX

CC This sequence encodes human caspase recruitment domain (CARD)-10. CARD proteins play roles in apoptotic and inflammatory signalling pathways. CARD-9, -10 and -11 participate in the network of interactions that modulate caspase activity. They are thought to be useful as modulating agents for regulating a variety of cellular processes including cell growth and cell death. CARD proteins and nucleic acids are useful for treating a disorder associated with inappropriate apoptosis or lymphocyte activation or for diagnosing subjects having or that are at risk of

CC developing a disorder associated with aberrant CARD-9, CARD-10 or CARD-11 expression or activity, such as cancer e.g. melanoma, autoimmune disease e.g. arthritis, or neurological disorders e.g. Alzheimer's disease

XX

CC Sequence 3949 BP; 724 A; 1222 C; 1319 G; 684 T; 0 U; 0 Other;

XX

Query Match 4.6%; Score 19; DB 6; Length 3949;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 GGACGAGGAGGAGGCTGCTG 174

DB 220 GGACGAGGAGGAGGCTGCTG 238

RESULT 14

ADE07581/C

ID ADE07581 standard; DNA; 5211 BP.

XX

AC ADE07581;

XX

DT 29-JAN-2004 (first entry)

XX

XX Novel coding sequence (useful for identifying genetic disorders) #647.

XX

XX novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder; gene; ds.

XX

OS unidentified.

XX

XX MO2003054152-A2.

XX

XX 03-JUL-2003.

XX

XX 10-DEC-2002; 2002WO-US039555.

XX

XX 10-DEC-2001; 2001US-0339739P.

XX

XX 11-DEC-2001; 2001US-0339433P.

XX

XX 14-MAR-2002; 2002US-0365091P.

XX

XX 14-MAR-2002; 2002US-0365384P.

XX

XX 12-APR-2002; 2002US-0372381P.

XX

XX 12-APR-2002; 2002US-0372615P.

XX

XX 22-APR-2002; 2002US-00128558.

XX

XX 24-APR-2002; 2002US-0376045P.

XX

XX (HYSE-) HYSEQ INC.

XX

XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao Qa, Wang J; Gosh W, Xue AJ, Wehrman T, Weng G, Zhou P, Dimanac RT, Wang Z; Ma Y, Wang D, Chen R, Xu C, Boyle BJ;

XX

XX WPI; 2003-569235/53.

XX

XX P-PSDB; ADE08492.

XX

XX New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.

XX

XX Claim 1; SEQ ID NO 647; 1177pp; English.

XX

XX The invention comprises the amino acid and coding sequences of novel CC proteins. The DNA and protein sequences of the invention are useful as: CC markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to CC compare with endogenous DNA sequences in patients to identify potential CC genetic disorders. The present DNA sequence represents a gene of the CC invention.

XX

XX Sequence 5211 BP; 1310 A; 1515 C; 1409 G; 977 T; 0 U; 0 Other;

XX

Query Match 4.6%; Score 19; DB 9; Length 5211;

Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 TCTACACCTGTGTCACCGG 314
1307 TCTACACCTGTGTCACCGG 1289

Search completed: March 21, 2004, 23:44:55
Job time : 261 secs

RESULT 15
AAZ22282/c
ID AAZ22282 standard; DNA; 5790 BP.

XX AAZ22282;

XX 06-DEC-1999 (first entry)

XX Nucleic acid sequence of KIAA380.

XX RGS; guanine nucleotide exchange factor; GEF; RGS domain; GAS; cancer;
KM G protein alpha subunit; cell proliferation; growth control; hemostasis;
KM morphogenesis; stress fiber formation; integrin-mediated interaction;
KM embryonic development; tumor cell growth; cell death; leukocyte homing;
KM bone resorption; clot retraction; db1 homology domain; mechanical stress;
KM pleckstrin homology domain; KIAA380; ss.

XX Homo sapiens.

XX WO9947557-A2.

XX 23-SEP-1999.

XX 18-MAR-1999; 99WO-US006051.

XX 18-MAR-1998; 98US-0078634P.

XX (ONYX-) ONYX PHARM INC.

XX Boliag G, Hart MJ, Roscoe W, Polakie P, Sternweis P, Kozasa T;
PI Jiang X;

XX WPI; 1999-571821/48.

XX P-PSDB; AAY41010.

PT New isolated RGS-GEF polypeptides, used to develop products for
modulating, e.g. cell proliferation and integrin-mediated interactions.

PS Example; Fig 13; 75bp; English.

XX The invention relates to isolated RGS-guanine nucleotide exchange factor
(GEF) polypeptides. The novel isolated RGS-GEF polypeptide consists of an
RGS domain of a GEF protein and does not comprise a db1 homology (DH)
domain or a pleckstrin homology (PH) domain. The RGS-GEF polypeptides can
be used for modulating an activity of a G protein alpha subunit (GAS).
XX The products can be used for the regulation of biological pathways in
which a RGS-GEF polypeptide is involved, particularly pathological
conditions, e.g. cell proliferation (e.g. cancer), morphogenesis, growth
control, stress fiber formation, and integrin-mediated interactions, such
as embryonic development, tumor cell growth and metastasis, programmed
cell death, hemostasis, leukocyte homing and activation, bone resorption,
clot retraction, and the response of cells to mechanical stress. The
XX products can also be used for detection, diagnosis and production of
transgenic animals. The present sequence represents the nucleic acid
sequence of KIAA380

XX Sequence 5790 BP; 1415 A; 1640 C; 1515 G; 1220 T; 0 U; 0 Other;

Query Match 4.6%; Score 19; DB 2; Length 5790;

Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 TCTACACCTGTGTCACCGG 314
1596 TCTACACCTGTGTCACCGG 1578

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 01:25:35 ; Search time 78 Seconds
(without alignments)
2966.853 Million cell updates/sec

Title: US-10-032-159A-15

Perfect score: 417

Sequence: 1 atggggggaactgtgcgcag.....ggctctcgttaaccacgann 417

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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2: /cgm2_6/prodata/2/ina/5B_COMB.seq:*
3: /cgm2_6/prodata/2/ina/5A_COMB.seq:*
4: /cgm2_6/prodata/2/ina/5B_COMB.seq:*
5: /cgm2_6/prodata/2/ina/PCTUS_COMB.seq:*
6: /cgm2_6/prodata/2/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18	4.3	39	4	US-08-693-234-23
C 2	18	4.3	48	1	US-08-276-852-35
C 3	18	4.3	48	1	US-08-133-011-107
C 4	18	4.3	48	1	US-08-322-730A-107
C 5	18	4.3	48	1	US-08-387-874-79
C 6	18	4.3	48	1	US-08-899-575-35
C 7	18	4.3	48	1	US-08-899-575-35
C 8	18	4.3	48	2	US-08-383-619-107
C 9	18	4.3	48	2	US-08-888-366-36
C 10	18	4.3	48	3	US-08-767-128-43
C 11	18	4.3	48	3	US-08-907-739-107
C 12	18	4.3	48	4	US-08-972-564-19
C 13	18	4.3	48	4	US-09-729-597-107
C 14	18	4.3	48	5	PCT-US93-08364-79
C 15	18	4.3	48	5	PCT-US95-00067-21
C 16	18	4.3	48	5	PCT-US95-08743-35
C 17	18	4.3	708	1	US-08-276-852-40
C 18	18	4.3	708	1	US-08-133-011-113
C 19	18	4.3	708	1	US-08-322-730A-113
C 20	18	4.3	708	1	US-08-387-874-86
C 21	18	4.3	708	1	US-08-899-575-40
C 22	18	4.3	708	1	US-08-899-575-40
C 23	18	4.3	708	2	US-08-383-619-113
C 24	18	4.3	708	3	US-08-907-739-113
C 25	18	4.3	708	4	US-09-729-597-113
C 26	18	4.3	708	5	PCT-US93-08364-86
C 27	18	4.3	708	5	PCT-US95-08743-40

C 28	18	4.3	4054	3	US-09-098-287A-9	Sequence 9, Appl
C 29	18	4.3	4054	4	US-09-445-649-9	Sequence 9, Appl
C 30	18	4.3	5292	2	US-08-793-610-3	Sequence 3, Appl
C 31	18	4.3	5292	2	US-08-793-610-2	Sequence 2, Appl
C 32	18	4.3	5323	2	US-08-793-610-1	Sequence 1, Appl
C 33	18	4.3	5364	2	US-08-793-610-4	Sequence 4, Appl
C 34	18	4.3	41100	4	US-09-755-665-46	Sequence 46, Appl
C 35	17	4.1	152	4	US-09-621-976-8569	Sequence 8569, Ap
C 36	17	4.1	469	4	US-09-621-976-15217	Sequence 15217, A
C 37	17	4.1	472	4	US-09-621-976-2762	Sequence 2762, Ap
C 38	17	4.1	516	1	US-08-438-753B-29	Sequence 29, Appl
C 39	17	4.1	516	1	US-08-443-883A-29	Sequence 29, Appl
C 40	17	4.1	516	2	US-08-631-328-29	Sequence 29, Appl
C 41	17	4.1	516	2	US-08-455-524B-29	Sequence 29, Appl
C 42	17	4.1	516	2	US-08-455-021B-29	Sequence 29, Appl
C 43	17	4.1	516	3	US-09-045-467-29	Sequence 29, Appl
C 44	17	4.1	516	4	US-08-616-904-5	Sequence 5, Appl
C 45	17	4.1	518	1	US-08-438-753B-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-08-693-234-23/c
; Sequence 23, Application US/08693234
; Patent No. 6596597
; GENERAL INFORMATION:
; APPLICANT: SODDYER, ET AL
; TITLE OF INVENTION: PROCESS FOR PREPARING A MULTICOMBINATORIAL LIBRARY OF VECTORS FOR
; FILE REFERENCE: P03144US0/BAS
; CURRENT APPLICATION NUMBER: US/08/693,234
; PRIOR APPLICATION NUMBER: PCT/FR95/00127
; PRIOR FILING DATE: 1995-02-02
; PRIOR APPLICATION NUMBER: FR 94 01519
; PRIOR FILING DATE: 1994-02-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Escherichia coli
US-08-693-234-23

Query Match 4.3%; Score 18; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 67 ATGAGAGCCACCGCCAC 84
Db 27 ATGAGAGCCACCGCCAC 10

RESULT 2
US-08-276-852-35/c
; Sequence 35, Application US/08276852
; Patent No. 5652138
; GENERAL INFORMATION:
; APPLICANT: Burton, Dennis R
; APPLICANT: Barbas, Carlos A
; APPLICANT: Lerner, Richard A
; TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSER: The Scripps Research Institute, Office of
; ADDRESSER: Patent Counsel
; STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220,
; STREET: Mail Drop TPC8
; CITY: La Jolla
; STATE: CA

COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Filting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRI452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-276-852-35

Query Match 4.3%; Score 18; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGGAGAGCCACCGCCAC 84
DB 31 ATGGAGAGCCACCGCCAC 14

RESULT 3
US-08-133-011-107/c
Sequence 107, Application US/08133011
Patent No. 5658727
GENERAL INFORMATION:
APPLICANT: Kang, Andray
APPLICANT: Barbas, Carlos
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
TITLE OF INVENTION: PHAGEMIDS
NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5658727th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133,011
FILING DATE: 08-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Filting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-133-011-107

Query Match 4.3%; Score 18; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGGAGAGCCACCGCCAC 84
DB 31 ATGGAGAGCCACCGCCAC 14

RESULT 4
US-08-322-730A-107/c
Sequence 107, Application US/08322730A
Patent No. 5759817
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
TITLE OF INVENTION: PHAGEMIDS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10550 No. 5759817th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,730A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bingham, Douglas A
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SCRO707P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-784-2937

TELEFAX: 619-784-9399
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-322-730A-107

Query Match 4.3%; Score 18; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
|||
DB 31 ATGAGAGCCACCGCCAC 14

RESULT 5

US-08-387-874-79/c
Sequence 79, Application US/08387874
Patent No. 5770356

GENERAL INFORMATION:

APPLICANT: Light, Paul L., II
APPLICANT: Lerner, Richard A.

TITLE OF INVENTION: PHAGEIDS COEXPRESSION A SURFACE
NUMBER OF INVENTION: RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN

NUMBER OF SEQUENCES: 97

CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of

STREET: 10666 No. 5770356th Torrey Pines Road, Suite 220,
STREET: Mail Drop 1PC8

CITY: La Jolla
STATE: CA

COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,874
FILING DATE: 22-FEB-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08364
FILING DATE: 03-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,369

FILING DATE: 04-SEP-1992
ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 303.1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:

LENGTH: 48 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO

ANTI-SENSE: NO
US-08-387-874-79

Query Match 4.3%; Score 18; DB 1; Length 48;

Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
|||
DB 31 ATGAGAGCCACCGCCAC 14

RESULT 6

US-08-899-575-35/c
Sequence 35, Application US/08899575
Patent No. 5770440

GENERAL INFORMATION:

APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F

APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES

TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170

CORRESPONDENCE ADDRESS:
ADDRESS: The Scripps Research Institute, Office of

STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop 1PC8

CITY: La Jolla
STATE: CA

COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994

APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148

FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:

LENGTH: 48 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO

ANTI-SENSE: NO
US-08-899-575-35

Query Match 4.3%; Score 18; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
|||
DB 31 ATGAGAGCCACCGCCAC 14

RESULT 7

US-08-899-575-35/c
Sequence 35, Application US/08899575
Patent No. 580440
GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 580440th Torrey Pines Road, Suite 220,
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-899-575-35

Query Match 4.3%; Score 18; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
DB 31 ATGAGAGCCACCGCCAC 14

RESULT 8
US-08-383-619-107/c
Sequence 107, Application US/08383619
Patent No. 595341
GENERAL INFORMATION:
APPLICANT: Kang, Argray
APPLICANT: Barbas, Carlos
APPLICANT: Lerner, Richard
TITLE OF INVENTION: HETEROLOGOUS RECEPTOR LIBRARIES USING
TITLE OF INVENTION: PHAGMIDS

NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: DOUGLAS A. BINGHAM
STREET: 11300 Sorrento Valley Road, Suite 200
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,619
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,680
FILING DATE:
APPLICATION NUMBER: US/07/683,602
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bingham, Douglas A.
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SCR0371P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1555
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-383-619-107

Query Match 4.3%; Score 18; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
DB 31 ATGAGAGCCACCGCCAC 14

RESULT 9
US-08-888-366-36/c
Sequence 36, Application US/08888366
Patent No. 5972656
GENERAL INFORMATION:
APPLICANT: Lopez, Osvaldo
APPLICANT: Wylie, Dwayne E.
APPLICANT: Wagner, Fred W.
TITLE OF INVENTION: Mercury Binding Polypeptides and Nucleotides Coding Therefore
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,366
FILING DATE: 03-JUL-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/187,407
FILING DATE: 27-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,542
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/493,299
FILING DATE: 14-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/324,392
FILING DATE: 14-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.39USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-888-366-36

Query Match 4.3%; Score 18; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGGAGAGCCACCGCCAC 84
DB 31 ATGGAGAGCCACCGCCAC 14

RESULT 10
US-08-767-128-43/C
Sequence 43, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION:
APPLICANT: WYLLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 03-JUN-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-767-128-43

Query Match 4.3%; Score 18; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGGAGAGCCACCGCCAC 84
DB 31 ATGGAGAGCCACCGCCAC 14

RESULT 11
US-08-907-739-107/C
Sequence 107, Application US/08907739
Patent No. 6235469
GENERAL INFORMATION:
APPLICANT: Kang, Angray
APPLICANT: Barbos, Carlos
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
TITLE OF INVENTION: PHAGEWIDS
NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 6235469th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,739
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/133,011
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-907-739-107

Query Match 4.3%; Score 18; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
Db 31 ATGAGAGCCACCGCCAC 14

RESULT 12
US-08-972-564-19/c
Sequence 19, Application US/08972564
Patent No. 6376170

GENERAL INFORMATION:
APPLICANT: Burton, Dennis R.
APPLICANT: Burioni, Roberto
APPLICANT: Williamson, R. Anthony
APPLICANT: Sanna, Pietro Paolo
TITLE OF INVENTION: LIGAND CAPTURE-DIRECTED SELECTION OF ANTIBODY
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/972,564
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/316,914
FILING DATE: October 3, 1994
ATTORNEY/AGENT INFORMATION:
NAME: LISA A. HAILE, P.H.D.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD-3809
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS

LOCATION: 1..48
US-08-972-564-19

Query Match 4.3%; Score 18; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
Db 31 ATGAGAGCCACCGCCAC 14

RESULT 13
US-09-729-597-107/c
Sequence 107, Application US/09729597
Patent No. 6468738

GENERAL INFORMATION:
APPLICANT: Kang, Angray
Barbas, Carlos
Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING PHAGEMIDS
NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of Patent Counsel
STREET: 10666 No. 6468738th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/729,597
FILING DATE: 04-Dec-2000
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/133,011
FILING DATE: 1994-09-29
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 107:
US-09-729-597-107

Query Match 4.3%; Score 18; DB 4; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
Db 31 ATGAGAGCCACCGCCAC 14

RESULT 14
PCT-US93-08364-79/c
; Sequence 79, Application PC/TUS9308364
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PHAGMIDS COEXPRESSION A SURFACE
; TITLE OF INVENTION: RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN
; NUMBER OF SEQUENCES: 97
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08364
; FILING DATE: 03-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,369
; FILING DATE: 04-SEP-1992
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; PCT-US93-08364-79

Query Match 4.3%; Score 18; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
DB 31 ATGAGAGCCACCGCCAC 14

RESULT 15
PCT-US95-00067-21/c
; Sequence 21, Application PC/TUS9500067
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HERPES
; TITLE OF INVENTION: SIMPLEX VIRUS AND METHODS THEREFOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Judas & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00067
; FILING DATE: 04-JAN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halle, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: PD-3229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..48
; PCT-US95-00067-21

Query Match 4.3%; Score 18; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 ATGAGAGCCACCGCCAC 84
DB 31 ATGAGAGCCACCGCCAC 14

Search completed: March 22, 2004, 03:19:52
Job time : 81 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Run on:      March 21, 2004, 23:45:00 ; Search time 3164 Seconds
              (without alignments)
              3935.692 Million cell updates/sec
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Title: US-10-032-159A-15

Sequence: 1 atgggggaactgtgcgcag.....ggtcctgttaaccacgmn 417

Scoring table: OLIGO_NUC

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hi

Total number of hits satisfying chosen parameters

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Database : EST:*

- 1: em_estdum:*
- 2: em_estdum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estop:*
- 7: em_estro:*
- 8: em_hc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_num:*
- 18: em_gss_inv:*
- 19: em_gss_dln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_pbg:*
- 27: em_gss_vrt:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	351	84.2	931	13	BU956261	ASBNCOURT
2	349	83.7	3015	29	AY1414357	Homo sapi
3	338	81.1	3015	29	AY1414358	Pan trogl
4	110	26.4	1141	10	BB867544	601443044

C	5	47	11.3	549	10	BF07981.9	BP07983.9	230513	MA
C	6	33	7.9	492	12	BQ031835	BQ031835	UI-1	-CP0-
C	7	33	7.9	806	10	BF100075	BF100075	601752245	
C	8	33	7.9	1600	11	AK086176	AK086176	Mus muscu	
C	9	33	7.9	2996	29	AY414359	AY414359	Mus muscu	
C	10	23	5.5	601	10	BE291786	BE291786	601084552	
C	11	21	5.0	478	28	AQ085003.4	AQ085003.4	1MAJFV.1	
C	12	21	5.0	514	12	BG090138	BG090138	u575b02.Y	
C	13	21	5.0	537	29	LB00728Y	LB00728Y	Leishmani	
C	14	21	5.0	576	28	AZ839378	AZ839378	2M0107F06	
C	15	21	5.0	655	12	BF649319	BF649319	603277822	
C	16	21	5.0	1024	13	BY702884	BY702884	BY702884	
C	17	21	5.0	1075	11	AK002346	AK002346	Mus muscu	
C	18	21	5.0	1104	29	AY402235	AY402235	Mus muscu	
C	19	20	4.8	1014	29	CNS01UDG	A167749	Feiradon	
C	20	19	4.6	234	14	W83246	W83246	mE27f11.r1	
C	21	19	4.6	299	9	A1622099	A1622099	486032G10	
C	22	19	4.6	299	9	AV122681	AV122681	AV122681	
C	23	19	4.6	360	9	AV193176	AV193176	AV193176	
C	24	19	4.6	370	10	BF018592	BF018592	ux79e11.Y	
C	25	19	4.6	371	28	AZ615770	AZ615770	1M0445H13	
C	26	19	4.6	381	12	BM076573	BM076573	TRESST-A00	
C	27	19	4.6	392	12	BG177337	BG177337	602689691	
C	28	19	4.6	409	10	BF507352	BF507352	UI-H-BM1-	
C	29	19	4.6	431	12	BJ178531	BJ178531	BJ178531	
C	30	19	4.6	433	12	BF140955	BF140955	gc31b07.Y	
C	31	19	4.6	438	14	CA389448	CA389447	gc509h05.Y	
C	32	19	4.6	444	10	AW829774	AW829774	r444c08.Y	
C	33	19	4.6	446	9	AA647911	AA647911	vt08f05.Y	
C	34	19	4.6	453	12	BF1740621	BF1740621	gc38a11.Y	
C	35	19	4.6	453	12	BM001080	BM001080	1031093A1	
C	36	19	4.6	471	29	CE605544	CE605544	tiGr-g98-	
C	37	19	4.6	484	14	CB727348	CB727348	AMGNMC.M	
C	38	19	4.6	494	12	BJ184852	BJ184852	BJ184852	
C	39	19	4.6	496	10	BF114874	BF114874	7187H01.X	
C	40	19	4.6	515	28	BH265897	BH265897	1006133C0	
C	41	19	4.6	519	12	BJ196726	BJ196726	BJ196726	
C	42	19	4.6	519	12	BJ197185	BJ197185	BJ197185	
C	43	19	4.6	519	12	BM877430	BM877430	iE94h09.Y	
C	44	19	4.6	527	28	AF106737	AF106737	AF106737	
C	45	19	4.6	537	12	BQ039741	BQ039741	gd02e05.Y	

ALIGNMENTS

```

RESULT 1      BU956261 LOCUS
DEFINITION    BU956261          931 bp   mRNA   linear   EST 21-OCT-2002
ACCESSION     AGCNCORT_10613482 NIH_MGC_107 Homo sapiens cDNA clone
VERSION       IMAGE:6729809 5' ,  mRNA sequence.
KEYWORDS      BU956261
SOURCE        BU956261.1  GR:24185833
ORGANISM      EST.
              Homo sapiens (human)
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 931)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL       National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT       Unpublished (1999)
               Contact: Robert Strausberg, Ph.D.
               Email: csagabs@mail.nih.gov
               Tissue Procurement: ATCC
               cDNA Library Preparation: Rubin Laboratory
               cDNA library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LINTL at:
               http://image.llnl.gov
               Place: LINC3053 row= 1 column: 16
               High quality sequence stop: 594.
```


COMMENT
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES
source
1. 3015
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
"1. 3015"
/gene="CARD14"
/locus_tag="HCM5197"

ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 4,2e-146; Length 3015;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGAAGTGTGCTCCGACAGGACTCCGACATCGACATGAGAGAGACACTGTGG 60
DB 1 ATGGGGGAAGTGTGCTCCGACAGGACTCCGACATCGACATGAGAGAGACACTGTGG 60
QY 61 GAGATGATGAGAGAGACAGGACAGGATGTAGAGCTGTGCTCCGACAGGACTGTGACC 120
DB 61 GAGATGATGAGAGAGACAGGACAGGATGTAGAGCTGTGCTCCGACAGGACTGTGACC 120
QY 121 CCTTACCTGGCCAGGACAGGATGTGCTGTGCTGACAGAGAGAGAGAGTGTGACACAGC 180
DB 121 CCTTACCTGGCCAGGACAGGATGTGCTGTGCTGACAGAGAGAGAGAGTGTGACACAGC 180
QY 181 CCCCAGCTGACCAACAGAGGATGTGCTGTGCTGATTTGCTGAGAGACTTCGAG 240
DB 181 CCCCAGCTGACCAACAGAGGATGTGCTGTGCTGATTTGCTGAGAGACTTCGAG 240
QY 241 GGGAGAGACGCGGACATGCGCTTCTCTGAGAGAGCTGAGAGTTCACAACTGTGACTTAC 300
DB 241 GGGAGAGACGCGGACATGCGCTTCTCTGAGAGAGCTGAGAGTTCACAACTGTGACTTAC 300
QY 301 ACCCTGTGTACACGCGGCTGACAGCTGATTTGACTTCAG 338
DB 301 ACCCTGTGTACACGCGGCTGACAGCTGATTTGACTTCAG 338

RESULT 4
LOCUS BE867544 1141 bp mRNA linear EST 20-OCT-2000
DEFINITION 601443043P1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847282 5', mRNA sequence.
ACCESSION BE867544
VERSION BE867544.1 GI:10316320
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1141)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
Plate: LIA9561 row: e column: 11
High quality sequence start: 4
High quality sequence stop: 269.
Location/Qualifiers
1. 1141
/organism="Homo sapiens"

FEATURES
source

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3847282"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6, site 1: NotI; site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."

ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 3.9e-40; Length 1141;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGAAGTGTGCTCCGACAGGACTCCGACATCGAGGACATGAGAGAGACACTGTGG 60
DB 161 ATGGGGGAAGTGTGCTCCGACAGGACTCCGACATCGAGGACATGAGAGAGACACTGTGG 220
QY 61 GAGATGATGAGAGAGACAGGACAGGATGTAGAGCTGTGCTCCGACAGGACTGTGACC 110
DB 221 GAGATGATGAGAGAGACAGGACAGGATGTAGAGCTGTGCTCCGACAGGACTGTGACC 270

RESULT 5
LOCUS BF079819 549 bp mRNA linear EST 18-OCT-2000
DEFINITION 230513 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BF079819
VERSION BF079819.1 GI:10873649
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
REFERENCE 1 (bases 1 to 549)
Fahnenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Perrea, G., Sultana, R., Quackenbush, J. and Keefe, J.W.
Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
JOURNAL MEDLINE
PUBMED 122213789
COMMENT Contact: Smith TPJ
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCAAGAGC
Plate: 47 row: M column: 12
Seq primer: ATTATGCTGACCTATAG.
Location/Qualifiers
1. 549
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9623"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 2P1G"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

FEATURES

source

ORIGIN

Query Match
11.3%; Score 47; DB 10; Length 549;

Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 AAGACGGGGCCATCGCTTCTGAGAGCCCTGAGTTCACACCC 290
|||||
314 AAGACGGGGCCATCGCTTCTGAGAGCCCTGAGTTCACACCC 360
|||||

RESULT 6
BQ031835/c 492 bp mRNA linear EST 27-MAR-2002
LOCUS UI-1-CFO-ach-c-03-0-UI.31 NCI CGAP P171 Mus musculus cDNA clone
DEFINITION UI-1-CFO-ach-c-03-0-UI.31, mRNA sequence.
ACCESSION BQ031835
KEYWORDS EST.
SOURCE BQ031835.1 GI:19767114
MUS musculus (house mouse)

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 492)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Dr. Minoru Ko, Dr. Janet Rosent, Dr. Janet

Rosent
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-49, >AT-richLow_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source Location/Qualifiers

1..492
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-1-CFO-ach-c-03-0-UI"
/tissue_type="Trophoblast"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP P171"
/notes="Organ: Placenta; Vector: pRTT3-Pac (Pharmacia) with
a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP P171 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pRTT3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are GTGG, ATCAT, GGAGT,
GGTGG. For additional information, contact: Bento Soares,
bento-soares@uiowa.edu
TAG_11505=Placenta mouse 11.5-12.5 days
TAG_LIB=UI-1-CFO
TAG_SEQ=ATCAT"

ORIGIN
Query Match 7.9%; Score 33; DB 12; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 CTCACCCCTACTGCGCCAGGCCAAGGTGCTG 147
|||||

DB 316 CTCACCCCTACTGCGCCAGGCCAAGGTGCTG 284

RESULT 7
BF100075 806 bp mRNA linear EST 19-OCT-2000
LOCUS 601752245F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3979883 5',
DEFINITION mRNA sequence.
ACCESSION BF100075
KEYWORDS EST.
SOURCE BF100075.1 GI:10882601
MUS musculus (house mouse)

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 806)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>

Plate: L1AM9174 row: j column: 12
High quality sequence, stop: 668.
FEATURES
source Location/Qualifiers

1..806
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3979883"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam1"
/notes="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 7.9%; Score 33; DB 10; Length 806;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 CTCACCCCTACTGCGCCAGGCCAAGGTGCTG 147
|||||
DB 418 CTCACCCCTACTGCGCCAGGCCAAGGTGCTG 450
|||||

RESULT 8
AK086176 1600 bp mRNA linear HTC 20-SEP-2003
LOCUS AK086176
DEFINITION Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched
library, clone: D93010J19 product: CASPASE RECRUITMENT DOMAIN
PROTEIN 14 (BCL10-INTERACTING MAGUK PROTEIN 2) (BIM2) [Mus
musculus], full insert sequence.

ACCESSION AK086176
VERSION AK086176.1 GI:26103277
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komoto, H., Akiyama, J., Nishi, K., Katsunari, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichannel sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
MEDLINE 11076861
PUBMED 11076861
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 11076861
PUBMED 11076861
REFERENCE 6
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hasegawa, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komoto, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numata, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shizaki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers
1. 1600
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="PANTOM_DB:D930010J19"
/db_xref="MGI:2423547"
/db_xref="taxon:10090"
/clone="D930010J19"

misc_feature
/tissue_type="head"
/clone_id="RIKEN full-length enriched mouse cDNA library"
/dev_stage="15 days embryo"
1. 1600
/note="CAPSASE RECRUITMENT DOMAIN PROTEIN 14 (BC10-INTERACTING MAGUK PROTEIN 2) (BIMP2) [Mus musculus] (SWISSPROT|Q99KFO, evidence: FASTA, 85.1%id, 76.9%length, match=2706 and 100% to the mouse sequence)"
ORIGIN
Query Match 7.9%; Score 33; DB 11; Length 1600;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 115 CTCACCCCTCTGCTGCGCCAGCCAGGTGCTG 147
Db 668 CTCACCCCTCTGCTGCGCCAGCCAGGTGCTG 720
RESULT 9
AY414359 2996 bp DNA linear GSS 17-DEC-2003
LOCUS Mus musculus CARD14 gene, VIRUTAL TRANSCRIPT, partial sequence.
DEFINITION AY414359
VERSION AY414359.1 GI:39770321
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
1 (bases 1 to 2996)
REFERENCE 1
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, J.J., Adams, M.D., and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
MEDLINE 14671302
PUBMED 14671302
REFERENCE 2 (bases 1 to 2996)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, J.J., Adams, M.D., and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
source
1. 2996
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1...>2996
/gene="CARD14"
/locus_tag="HCM5197"
ORIGIN
Query Match 7.9%; Score 33; DB 29; Length 2996;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 115 CTCACCCCTCTGCTGCGCCAGCCAGGTGCTG 147
Db 115 CTCACCCCTCTGCTGCGCCAGCCAGGTGCTG 147
RESULT 10
BE291786 601 bp mRNA linear EST 13-JUL-2000
LOCUS BE291786
DEFINITION 601084552P1 NCI_GAP_Mam6 Mus musculus cDNA clone IMAGE:3498685 5',

ACCESSION BE291786 mRNA sequence.
 VERSION BE291786.1 GI:9173747
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 601)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@ds-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1M8554 row: h column: 14
 High quality sequence stop: 582.
 Location/Qualifiers
 1..601
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:3498685"
 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="MDH10B"
 /clone_lib="NCI-CGAP_Mame"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt: Site: 2; NCI: Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

ORIGIN
 Query Match 5.5%; Score 23; DB 10; Length 601;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 AGCCTGAAGTTCACACCCCTGA 293
 |||||
 DB 10 AGCCTGAAGTTCACACCCCTGA 32

RESULT 11 478 bp DNA linear GSS 25-MAY-2001
 A0850034/c LMAJFV1 lm53a09.y1 Leishmania major FV1 random genomic library
 DEFINITION Leishmania major genomic clone LMAJFV1 lm53a09 5' similar to
 TR:92188 P92188 PROTEASOME 29 KD SUBUNIT'', genomic survey
 sequence.
 A0850034
 A0850034.1 GI:6054682
 GSS.
 Leishmania major
 Leishmania major
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Leishmania.
 1 (bases 1 to 478)
 Akopyants,N.S., Clifton,S.W., Martin,J., Pape,D., Wylie,T., Li,L.,
 Kissinger,J.C., Roos,D.S. and Beverley,S.M.
 A survey of the Leishmania major Friedlin strain V1 genome by
 shotgun sequencing: a resource for DNA microarrays and expression
 profiling
 JOURNAL Mol. Biochem. Parasitol. 113 (2), 337-340 (2001)
 MEDLINE 21192559
 PUBMED 11295190

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED

COMMENT Other GSSs: lm53a09.x1
 Contact: Akopyants, NS / Beverley, SM
 Washu Leishmania Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 Library construction: Natalia S. Akopyants, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 If using this information please cite:
 N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
 Friedlin strain V1 genome by shotgun sequencing' and the Washington
 University Genome Sequencing Center for information on obtaining
 clone material please contact: Natalia S. Akopyants Ph.D.
 (natalia@borcim.wustl.edu) and/or Stephen M. Beverley Ph.D.
 (beverley@borcim.wustl.edu)
 Seq primer: -40RP from Gibco
 Class: shotgun
 High quality sequence stop: 369.
 Location/Qualifiers
 1..478
 /organism="Leishmania major"
 /mol_type="genomic DNA"
 /strain="Friedlin strain V1"
 /db_xref="taxon:5664"
 /clone="LMAJFV1 lm53a09"
 /lab_host="TOP10 (Invitrogen)"
 /clone_lib="Leishmania major FV1 random genomic library"
 /note="Vector: pZero-2 (Invitrogen); Site: 1; EcoRV;
 Genomic DNA was isolated from stationary phase cells. For
 this library, DNA was sheared to give a tight size
 distribution of 1-1.5kb fragments, blunt-ended with T4 DNA
 polymerase, dephosphorylated with Shrimp Alkaline
 Phosphatase and ligated into pZero-2 vector's EcoRV site."

ORIGIN
 Query Match 5.0%; Score 21; DB 28; Length 478;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 GGACGAGAGAGAGTGTCTGA 176
 |||||
 DB 149 GGACGAGAGAGAGTGTCTGA 129

RESULT 12 514 bp mRNA linear EST 26-JAN-2001
 BG090138 u57502.y1 Soares mouse NGCB bccl1 Mus musculus cDNA clone
 LOCUS IMAGE:333189 5', mRNA sequence.
 DEFINITION IMAGE:333189 5', mRNA sequence.
 ACCESSION BG090138
 VERSION BG090138.1 GI:12572701
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 514)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@ds-remail.nih.gov
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 NC1:1076063
 Seq primer: -40RP from Gibco
 High quality sequence stop: 475.
 Location/Qualifiers
 1..514
 /organism="Mus musculus"

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 SOURCE


```

/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:333189"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Scars_mouse_NK6B_bcell"
/notes="Organ: germinal B-cell; Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer 15'
TGTATCCATCTGAGGAGGAGGCGCGCTGTTTCTTTTCTTTTCTTTTCTTTT
T 3'; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized; constructed by Benito Soares and
M.Fatima Bonaldi."

```

ORIGIN

Query Match 5.0%; Score 21; DB 12; Length 514;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 CTCACCCCTACCTGCGCCAG 135
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 335 CTCACCCCTACCTGCGCCAG 355

RESULT 13

L8007BY

LOCUS L8007BY 537 bp DNA linear GSS 29-APR-2000
 DEFINITION Leishmania major Friedlin cosmid L8007.2 t7 end-sequence, similar
 to TBR131148 Trypanosoma brucei rhodesiense mRNA. . . .
 N=952, Prob=1.6e-69; TR:P92188 P92188 PROTEASOME 29 KD SUBUNIT
 (BC. . . N=551, Prob=1.2e-78, genomic survey sequence.
 AL354405
 AL354405.1 GI:7672051

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Leishmania major
 Leishmania major
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Leishmania.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 1 (bases 1 to 537)
 Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and
 Smith,D.E.
 A physical map of the Leishmania major Friedlin genome
 Genome Res. 8 (2), 135-145 (1998)
 9477341

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 2 (bases 1 to 537)
 Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and
 Barrell,B.G.
 Direct Submission
 Submitted (28-APR-2000) Leishmania major Friedlin genome sequencing
 Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 alicat@sanger.ac.uk
 see http://www.ebi.ac.uk/parasites/leish.html
 details of Leishmania sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/L_major/
 The cDNA t7 primer sequence can be obtained from acc. no. US9231.

COMMENT

FEATURES
 source

```

1..537
/organism="Leishmania major"
/mol_type="genomic DNA"
/strain="Friedlin"
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ORIGIN

Query Match 5.0%; Score 21; DB 29; Length 537;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 GGACGAGAGAGTGTCTGCA 176

Db 397 GGACGAGAGAGTGTCTGCA 417
 |||||

RESULT 14 576 bp DNA linear GSS 20-FEB-2001
 A2829378
 2M010706F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
 LOCUS clone UUCG2M010706 F, genomic survey sequence.
 DEFINITION

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 1 (bases 1 to 576)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std. Error: 0.00
 Plate: 0107 row: F column: 06
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 576.

FEATURES

source

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1..576
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0107F06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"  

/clone_lib="Mouse 10kb plasmid UUCG1M library"  

/notes="Vector: PWD42nv; Purified genomic DNA from M.  

musculus C57BL/6J (male) was obtained from the Jackson  

Laboratory Mouse DNA Resource  

(http://www.jax.org/resources/documents/dnares/). The DNA  

was hydrodynamically sheared by repeated passage through a  

0.005 inch orifice at constant velocity. The sheared DNA  

was blunt end-repaired with T4 DNA polymerase and T4  

polynucleotide kinase. Adaptor oligonucleotides were  

ligated to the blunt ends in high molar excess. The  

adaptor DNA was purified and size-selected for a 9.5 to  

10.5 kb range using preparative agarose gel  

electrophoresis. Vector DNA was prepared from a derivative  

of PWD42 (g114732114|gb|AF129072.1), a copy-number  

inducible derivative of plasmid R1. The vector was ligated  

with adaptors complementary to the insert adaptors and  

purified. The sheared, adaptor mouse DNA was annealed to  

adaptor vector DNA, and transformed into  

chemically-competent E. coli XL10-Gold (Stratagene) cells  

and selected for ampicillin resistance."

```

ORIGIN

Query Match 5.0%; Score 21; DB 28; Length 576;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 CTCACCAACAGCGCATGCGG 207

Db 232 CTCACCCACAGCGCCATGCGG 212

RESULT 15

BI649379

655 bp mRNA linear EST 12-SEP-2001

603277822P1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5318165 5',

mRNA sequence.

BI649378

BI649379.1 GI:15563615

EST.

Mus musculus (house mouse)

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cga@dbp-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LLAM1806 row: 1 column: 06

High quality sequence start: 4

High quality sequence stop: 653.

Location/Qualifiers

1..655

/organism="Mus musculus"

/mol_type="mRNA"

/strain="129,C57BL/6J,FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5318165"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Mam3"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;

Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH

Reference for transgenic model: Xu et al., Nature Genetics

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

Search completed: March 22, 2004, 03:12:48
Job time: 3173 secs

ORIGIN

Query Match 5.0%; Score 21; DB 12; Length 655;

Best Local Similarity 100.0%; Pred. No. 87; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 CTCACCCCTTACCTGCGCCAG 135

DB 442 CTCACCCCTTACCTGCGCCAG 462

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 22, 2004, 00:35:25 ; Search time 322 Seconds
(without alignments)
4790.519 Million cell updates/sec

Title: US-10-032-159A-15

Perfect score: 417
Sequence: 1 atcggggggaactgtgcgcag.....ggctccgttaaccacagm 417

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2438257 seqs, 1849576744 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	417	100.0	417	US-10-032-159A-15	Sequence 15, Appl
2	415	99.5	3417	US-09-767-215-4	Sequence 7, Appl
3	351	84.2	3012	US-09-767-215-3	Sequence 3, Appl
4	351	84.2	3766	US-10-104-047-315	Sequence 315, App
5	351	84.2	3931	US-09-767-215-1	Sequence 1, Appl
6	276	26.4	276	US-10-032-159A-17	Sequence 17, Appl
7	110	26.4	1141	US-10-032-159A-37	Sequence 37, Appl
8	22	5.3	509	US-10-027-632-280760	Sequence 280760,
9	22	5.3	509	US-10-027-632-280761	Sequence 280761,
10	20	4.8	534	US-10-282-122A-25923	Sequence 25923, A
11	19	4.6	867	US-09-821-831-3	Sequence 3, Appl
12	19	4.6	3096	US-09-798-412-9	Sequence 9, Appl
13	19	4.6	3096	US-10-325-917-9	Sequence 9, Appl
14	19	4.6	3259	US-10-388-934-557	Sequence 557, App
15	19	4.6	3260	US-09-821-831-1	Sequence 1, Appl

16	19	4.6	3949	US-09-798-412-7	Sequence 7, Appl
17	19	4.6	3949	US-10-325-917-7	Sequence 7, Appl
18	19	4.6	5790	US-10-134-102-7	Sequence 10, Appl
19	19	4.6	1163020	US-10-398-221-10	Sequence 10, Appl
20	19	4.6	3011208	US-10-398-221-2058	Sequence 2058, Ap
21	18	4.3	48	US-10-079-802-19	Sequence 19, Appl
22	18	4.3	48	US-10-016-986-35	Sequence 35, Appl
23	18	4.3	48	US-10-273-973-107	Sequence 107, App
24	18	4.3	708	US-10-016-986-40	Sequence 40, Appl
25	18	4.3	708	US-10-273-973-113	Sequence 113, App
26	18	4.3	908	US-10-424-599-82332	Sequence 82332, A
27	18	4.3	984	US-10-282-122A-31670	Sequence 31670, A
28	18	4.3	1830	US-10-156-761-7245	Sequence 7245, Ap
29	18	4.3	2390	US-10-221-278-81	Sequence 81, Appl
30	18	4.3	2390	US-10-119-926-35	Sequence 35, Appl
31	18	4.3	2390	US-10-291-172-81	Sequence 81, Appl
32	18	4.3	4054	US-10-321-195-9	Sequence 9, Appl
33	18	4.3	7654	US-10-006-773-1	Sequence 1, Appl
34	18	4.3	7654	US-10-006-771A-1	Sequence 1, Appl
35	18	4.3	41100	US-09-755-665-46	Sequence 46, Appl
36	18	4.3	9025608	US-10-156-761-1	Sequence 1, Appl
37	17	4.1	60	US-09-908-975-11168	Sequence 11168, A
38	17	4.1	130	US-09-994-228-53	Sequence 53, Appl
39	17	4.1	130	US-09-994-228-54	Sequence 54, Appl
40	17	4.1	252	US-10-156-761-5536	Sequence 5536, Ap
41	17	4.1	272	US-09-867-701-5725	Sequence 5725, Ap
42	17	4.1	295	US-10-424-599-117090	Sequence 117090,
43	17	4.1	362	US-09-864-761-33007	Sequence 33007, A
44	17	4.1	385	US-09-918-995-37596	Sequence 37596, A
45	17	4.1	435	US-10-425-114-20661	Sequence 20661, A

ALIGNMENTS

RESULT 1
US-10-032-159A-15
Sequence 15, Application US/10032159A
Publication No. US20020164703A1
GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032.159A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,457
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 417
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(417)
FEATURE:
NAME/KEY: misc_feature
LOCATION: 416, 417
OTHER INFORMATION: n = A,T,C or G
US-10-032-159A-15

Query Match 100.0%; Score 417; DB 13; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.3e-209;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 ATCGGGGAAGCTGTGCGGAGGAGCTCGGAGCTGAGCGAGTGAAGAGAGACTGTGG 60
1 ATCGGGGAAGCTGTGCGGAGGAGCTCGGAGCTGAGCGAGTGAAGAGAGACTGTGG 60

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QY 61 GAGATGATGAGAGCCACCGCCACAGATTCGTAGCTGATCTGCCCCAGCCGCTCAC 120
DB 61 GAGATGATGAGAGCCACCGCCACAGATTCGTAGCTGATCTGCCCCAGCCGCTCAC 120
QY 121 CCTTACTGCGCCAGCCAGAGGTGTGTGCGCAGCTGAGACGAGAGAGAGGTGTGTGAGC 180
DB 121 CCTTACTGCGCCAGCCAGAGGTGTGTGCGCAGCTGAGACGAGAGAGAGGTGTGTGAGC 180
QY 181 CCCCAGCTCACCAACAGCGCCCATGTGCGGCGCCGACCTTGCTGATTTGCTGAGACTGGA 240
DB 181 CCCCAGCTCACCAACAGCGCCCATGTGCGGCGCCGACCTTGCTGATTTGCTGAGACTGGA 240
QY 241 GGGAGAGAACGGGGCCATGCTTCTCTGAGAGCTGGAAGTTCCACAACCTGACCTTAC 300
DB 241 GGGAGAGAACGGGGCCATGCTTCTCTGAGAGCTGGAAGTTCCACAACCTGACCTTAC 300
QY 301 ACCCTGCTCACCGGCGCTGACGCTGATGTGACTTGAATTGAGCGGTGAGAGCTCC 360
DB 301 ACCCTGCTCACCGGCGCTGACGCTGATGTGACTTGAATTGAGCGGTGAGAGCTCC 360
QY 361 GACTTGAACGGTTTGGCAGGCACTTCTAGGAACCTCAGGCTCTGTGTAACCCAGNN 417
DB 361 GACTTGAACGGTTTGGCAGGCACTTCTAGGAACCTCAGGCTCTGTGTAACCCAGNN 417

RESULT 2
US-09-767-215-4
; Sequence 4, Application US/09767215
; Patent No. US20020081636A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-142001
; CURRENT APPLICATION NUMBER: US/09/767,215
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/181,159
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3417)
; US-09-767-215-4

Query Match 99.5%; Score 415; DB 9; Length 3417;
Best Local Similarity 100.0%; Pred. No. 1.1e-208;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGAACTGTGCGCGAGGAACTCCGCACTCAGGCACTTGGAGAGAGCACTGTGG 60
DB 1 ATGGGGGAACTGTGCGCGAGGAACTCCGCACTCAGGCACTTGGAGAGAGCACTGTGG 60
QY 61 GAGATGATGAGAGCCACCGCCACAGATTCGTAGCTGATCTGCCCCAGCCGCTCAC 120
DB 61 GAGATGATGAGAGCCACCGCCACAGATTCGTAGCTGATCTGCCCCAGCCGCTCAC 120
QY 121 CCTTACTGCGCCAGCCAGAGGTGTGTGCGCAGCTGAGACGAGAGAGGTGTGTGAGC 180
DB 121 CCTTACTGCGCCAGCCAGAGGTGTGTGCGCAGCTGAGACGAGAGAGGTGTGTGAGC 180
QY 181 CCCCAGCTCACCAACAGCGCCCATGTGCGGCGCCGACCTTGCTGATTTGCTGAGACTGGA 240
DB 181 CCCCAGCTCACCAACAGCGCCCATGTGCGGCGCCGACCTTGCTGATTTGCTGAGACTGGA 240
QY 241 GGGAGAGAACGGGGCCATGCTTCTCTGAGAGCTGGAAGTTCCACAACCTGACCTTAC 300
DB 241 GGGAGAGAACGGGGCCATGCTTCTCTGAGAGCTGGAAGTTCCACAACCTGACCTTAC 300
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QY 301 ACCCTGCTCACCGGCGCTGACGCTGATGTGACTTGAATTGAGCGGTGAGAGCTCC 360
DB 301 ACCCTGCTCACCGGCGCTGACGCTGATGTGACTTGAATTGAGCGGTGAGAGCTCC 360
QY 361 GACTTGAACGGTTTGGCAGGCACTTCTAGGAACCTCAGGCTCTGTGTAACCCAG 415
DB 361 GACTTGAACGGTTTGGCAGGCACTTCTAGGAACCTCAGGCTCTGTGTAACCCAG 415

RESULT 3
US-09-767-215-3
; Sequence 3, Application US/09767215
; Patent No. US20020081636A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
; FILE REFERENCE: 07334-142001
; CURRENT APPLICATION NUMBER: US/09/767,215
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/181,159
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3012
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-767-215-3

Query Match 84.2%; Score 351; DB 9; Length 3012;
Best Local Similarity 100.0%; Pred. No. 6.3e-175;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGAACTGTGCGCGAGGAACTCCGCACTCAGGCACTTGGAGAGAGCACTGTGG 60
DB 1 ATGGGGGAACTGTGCGCGAGGAACTCCGCACTCAGGCACTTGGAGAGAGCACTGTGG 60
QY 61 GAGATGATGAGAGCCACCGCCACAGATTCGTAGCTGATCTGCCCCAGCCGCTCAC 120
DB 61 GAGATGATGAGAGCCACCGCCACAGATTCGTAGCTGATCTGCCCCAGCCGCTCAC 120
QY 121 CCTTACTGCGCCAGCCAGAGGTGTGTGCGCAGCTGAGACGAGAGAGGTGTGTGAGC 180
DB 121 CCTTACTGCGCCAGCCAGAGGTGTGTGCGCAGCTGAGACGAGAGAGGTGTGTGAGC 180
QY 181 CCCCAGCTCACCAACAGCGCCCATGTGCGGCGCCGACCTTGCTGATTTGCTGAGACTGGA 240
DB 181 CCCCAGCTCACCAACAGCGCCCATGTGCGGCGCCGACCTTGCTGATTTGCTGAGACTGGA 240
QY 241 GGGAGAGAACGGGGCCATGCTTCTCTGAGAGCTGGAAGTTCCACAACCTGACCTTAC 300
DB 241 GGGAGAGAACGGGGCCATGCTTCTCTGAGAGCTGGAAGTTCCACAACCTGACCTTAC 300
QY 301 ACCCTGCTCACCGGCGCTGACGCTGATGTGACTTGAATTGAGCGGTGAGAGCTCC 360
DB 301 ACCCTGCTCACCGGCGCTGACGCTGATGTGACTTGAATTGAGCGGTGAGAGCTCC 360

RESULT 4
US-10-104-047-315
; Sequence 315, Application US/10/104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 315
LENGTH: 3766
TYPE: DNA
ORGANISM: Homo sapiens
US-10-104-047-315

Query Match
Best Local Similarity 100.0%; Score 351; DB 15; Length 3766;
Pred. No. 6.2e-175;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGAACTGTGCGGAGGAACTCCGACTTCACGGCACTGAGAGAGACTGTGG 60
DB 192 ATGGGGGAACTGTGCGGAGGAACTCCGACTTCACGGCACTGAGAGAGACTGTGG 251
QY 61 GAGATGATGAGAGCCACCGCCACAGAGATCGTACGTGATGTGCCACCGCCTCAC 120
DB 252 GAGATGATGAGAGCCACCGCCACAGAGATCGTACGTGATGTGCCACCGCCTCAC 311
QY 121 CCTTACTGCGCCAGGCGCAAGGTCGTGCGCAGCTGAGAGAGAGAGTGTGCACAGC 180
DB 312 CCTTACTGCGCCAGGCGCAAGGTCGTGCGCAGCTGAGAGAGAGAGTGTGCACAGC 371
QY 181 CCCCCTCACCACCAAGCCGCTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 372 CCCCCTCACCACCAAGCCGCTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
QY 241 GGGAGAACGGGGCCATCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 432 GGGAGAACGGGGCCATCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
QY 301 ACCCTGTCAACGGGCTGACAGCTGATGTTGACTTCAAGTACCTTAAGCGGT 351
DB 492 ACCCTGTCAACGGGCTGACAGCTGATGTTGACTTCAAGTACCTTAAGCGGT 542

RESULT 5
US-09-767-215-1

Sequence 1, Application US/09767215
Patent No. US2002081636A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
FILE REFERENCE: 07334-142001
CURRENT APPLICATION NUMBER: US/09/767,215
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/181,159
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 3931
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (207)...(3218)
US-09-767-215-1

Query Match
Best Local Similarity 100.0%; Score 351; DB 9; Length 3931;
Pred. No. 6.1e-175;
Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGAACTGTGCGGAGGAACTCCGACTTCACGGCACTGAGAGAGACTGTGG 60
DB 207 ATGGGGGAACTGTGCGGAGGAACTCCGACTTCACGGCACTGAGAGAGACTGTGG 266
QY 61 GAGATGATGAGAGCCACCGCCACAGAGATCGTACGTGATGTGCCACCGCCTCAC 120
DB 267 GAGATGATGAGAGCCACCGCCACAGAGATCGTACGTGATGTGCCACCGCCTCAC 326
QY 121 CCTTACTGCGCCAGGCGCAAGGTCGTGCGCAGCTGAGAGAGAGAGAGTGTGCACAGC 180

DB 327 CCTTACTGCGCCAGGCGCAAGGTCGTGCGCAGCTGAGAGAGAGAGTGTGCACAGC 386
QY 181 CCCCCTCACCACCAAGCCGCTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 387 CCCCCTCACCACCAAGCCGCTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 446
QY 241 GGGAGAACGGGGCCATCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 447 GGGAGAACGGGGCCATCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 506
QY 301 ACCCTGTCAACGGGCTGACAGCTGATGTTGACTTCAAGTACCTTAAGCGGT 351
DB 507 ACCCTGTCAACGGGCTGACAGCTGATGTTGACTTCAAGTACCTTAAGCGGT 557

RESULT 6
US-10-032-159A-17

Sequence 17, Application US/10032159A
Publication No. US20020164703A1
GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.
TITLE OF INVENTION: CARD-DOMAIN CONTAINING POLYPEPTIDES,
ENCODING NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: P-LJ 5100
CURRENT APPLICATION NUMBER: US/10/032,159A
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 60/257,457
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 276
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(276)
US-10-032-159A-17

Query Match
Best Local Similarity 100.0%; Score 276; DB 13; Length 276;
Pred. No. 2.9e-135;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 GAGGAGACACTGTGGGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 105
DB 1 GAGGAGACACTGTGGGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 106 CCGAGCGGCTCACCCCTTACTGCGCCAGGCGCAAGGTCGTGCGCAGCTGAGAGAG 165
DB 61 CCGAGCGGCTCACCCCTTACTGCGCCAGGCGCAAGGTCGTGCGCAGCTGAGAGAG 120
QY 166 GAGGTGCTGACAGCCCGGCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 225
DB 121 GAGGTGCTGACAGCCCGGCTTACCAAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 226 TTGCTGAAGACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 285
DB 181 TTGCTGAAGACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 286 AACCTGACGCTTACACCTTGTGTCACCGGCGCTGAG 321
DB 241 AACCTGACGCTTACACCTTGTGTCACCGGCGCTGAG 276

RESULT 7
US-10-032-159A-37

Sequence 37, Application US/10032159A
Publication No. US20020164703A1
GENERAL INFORMATION:
APPLICANT: Pawlowski, Krzysztof
APPLICANT: Reed, John C.

PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 7614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25923
LENGTH: 534
TYPE: DNA
ORGANISM: Mycobacterium avium
US-10-282-122A-25923

Query Match 4.8%; Score 20; DB 12; Length 534;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 TGGTCACCGGCTGCAGCCT 324
|||||
DB 290 TGGTCACCGGCTGCAGCCT 309

RESULT 11
US-09-821-831-3/c
Sequence 3, Application US/09821831
Patent No. US20020137188A1
GENERAL INFORMATION:
APPLICANT: Bartlett, Perry Francis
APPLICANT: Coulson, Elizabeth Jane
APPLICANT: Fieldew, Katrina
APPLICANT: Baca, Manuel
APPLICANT: Kilpatrick, Trevor
APPLICANT: Surindar, Cheema
TITLE OF INVENTION: Method of Modulating Cell Survival and
FILE REFERENCE: 3206.1001-000
CURRENT APPLICATION NUMBER: US/09/821,831
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/AU93/00860
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: AU P60701
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: AU P6351
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: AU P6353
PRIOR FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 867
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic CDNA sequence of rat
NAME/KEY: CDS
LOCATION: (115)...(867)
US-09-821-831-3

Query Match 4.6%; Score 19; DB 9; Length 867;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 AGGAACCTCAGGCTCCTGG 406
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DB 771 AGGAACCTCAGGCTCCTGG 753

RESULT 12
US-09-798-412-9

Sequence 9, Application US/09798412
Publication No. US20030109428A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
FILE REFERENCE: 07334-327001
CURRENT APPLICATION NUMBER: US/09/798,412
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 09/728,260
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/685,791
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/513,904
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 09/507,533
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US 60/168,780
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 3096
TYPE: DNA
ORGANISM: Homo sapiens
US-09-798-412-9

Query Match 4.6%; Score 19; DB 10; Length 3096;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 GGACGAGGAGAGGTGCTG 174
|||||
DB 180 GGACGAGGAGAGGTGCTG 198

RESULT 13
US-10-325-917-9
Sequence 9, Application US/10325917
Publication No. US20030113787A1
GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
FILE REFERENCE: 07334-327001
CURRENT APPLICATION NUMBER: US/10/325,917
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US/09/798,412
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 09/728,260
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/685,791
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/513,904
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 09/507,533
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: US 60/168,780
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 3096
TYPE: DNA
ORGANISM: Homo sapiens
US-10-325-917-9

Query Match 4.6%; Score 19; DB 14; Length 3096;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 156 GGACGAGGAGAGGTGCTG 174
|||||

DB 180 GGACGAGAGAGGTGCTG 198

RESULT 14

US-10-388-934-557/c
Sequence 557, Application US/10388934
Publication No. US20040005547A1

GENERAL INFORMATION:

APPLICANT: Boess, Franziska
APPLICANT: Suter-Dick, Laura
APPLICANT: Wolf, Detlef

TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
FILE REFERENCE: 21169

CURRENT APPLICATION NUMBER: US/10/388,934
CURRENT FILING DATE: 2003-03-14

PRIOR APPLICATION NUMBER: 02005336.9
PRIOR FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: 02015657.6
PRIOR FILING DATE: 2002-07-17

NUMBER OF SEQ ID NOS: 862
SOFTWARE: PatentIn version 3.1

SEQ ID NO 557
LENGTH: 3259

TYPE: DNA

ORGANISM: Rattus norvegicus (No. US20040005547A1way rat)
US-10-388-934-557

Query Match

Best Local Similarity 4.6%; Score 19; DB 15; Length 3259;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 AGGAACTCAGGCTCCTGG 406
DB 770 AGGAACTCAGGCTCCTGG 752

US-09-821-831-1/c

RESULT 15

US-09-821-831-1/c
Sequence 1, Application US/09821831
Patent No. US20020137188A1

GENERAL INFORMATION:

APPLICANT: Bartlett, Perry Francis
APPLICANT: Coulson, Elizabeth Jane
APPLICANT: Fieldew, Katrina

APPLICANT: Baca, Manuel
APPLICANT: Kilpatrick, Trevor

APPLICANT: Surindar, Cheema
TITLE OF INVENTION: Method of Modulating Cell Survival and

FILE REFERENCE: 3206.1001-000
CURRENT APPLICATION NUMBER: US/09/821,831
CURRENT FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: PCT/AU99/00860
PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: AU PQ0701
PRIOR FILING DATE: 1999-06-01

PRIOR APPLICATION NUMBER: AU PP6351
PRIOR FILING DATE: 1998-10-07

PRIOR APPLICATION NUMBER: AU PP6353
PRIOR FILING DATE: 1998-10-06

NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1
LENGTH: 3260

TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Synthetic CDNA Sequence of Human
NAME/KEY: CDS
LOCATION: (115)...(1389)
US-09-821-831-1

Query Match

4.6%; Score 19; DB 9; Length 3260;

Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 388 AGGAACTCAGGCTCCTGG 406

DB 771 AGGAACTCAGGCTCCTGG 753

Search completed: March 22, 2004, 03:18:38
Job time : 344 secs